

Access DB# 32383

## SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_  
Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

**FOR OFFICIAL USE ONLY**

\*\*\*\*\*

## STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>Ed Veen - Jaly</u>	NA Sequence (#) <u>4</u>	STN _____
Searcher Phone #: <u>308-4501</u>	AA Sequence (#) _____	Dialog _____
Searcher Location: <u>Biotec Lib.</u>	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>1/4/01</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>1/17/01</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <u>AB5501</u>
Clerical Prep Time: <u>5 mi</u>	Patent Family _____	WWW/Internet _____
Online Time: <u>2 mi</u>	Other _____	Other (specify) _____



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2000, 19:06:42 ; Search time 6198.48 Seconds

(without alignments)  
695.102 Million cell updates/sec

Title: US-09-180-798-30  
Perfect score: 1063  
Sequence: 1 tcgaccacagctccgacga.....tgcaaaaaaaaaaaaaa 1063

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4857316 seqs, 202661650 residues

Total number of hits satisfying chosen parameters: 9714632

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

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106: gb\_gss14:\*  
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108: gb\_gss16:\*  
109: gb\_gss16:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result

8  
Query

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
1	465.8	43.8	469	63	A1992868	A1992868 701493826
2	395.4	37.2	556	63	R89998	R89998 16353 lambd
3	373	35.1	442	42	A1100481	A1100481 34856 Lam
4	358	33.7	360	42	A1100685	A1100685 33806 Lam
5	349.4	32.9	364	42	A1100683	A1100683 33804 Lam
6	336.8	31.7	534	33	AA394359	AA394359 25942 Lam
7	332	31.2	348	42	A1100682	A1100682 33803 Lam
8	329.2	31.0	401	37	AA712221	AA712221 31949 Lam
9	327.8	30.8	353	23	H37300	H37300 15429 Lambd
10	318.2	29.9	608	81	AA443205	AA443205 EST308135
11	317.2	29.8	720	64	AM031110	AM031110 EST274417
12	314.6	29.6	339	42	A1100679	A1100679 33800 Lam
13	302.4	28.4	447	23	H36800	H36800 14929 Lambd
14	301.4	28.4	336	23	H37296	H37296 15425 Lambd
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16	297.6	28.0	657	80	AM350720	AM350720 GM210009A
17	296.8	27.9	511	74	AM221278	AM221278 EST287747
18	293.4	27.6	714	64	AM030188	AM030188 EST273443
19	292.6	27.5	336	42	A1100680	A1100680 33801 Lam
20	286.8	27.0	336	20	Z34187	Z34187 ATTS3221 Ve
21	281.6	26.5	334	23	H37195	H37195 15324 Lambd
22	280	26.3	695	64	AM038168	AM038168 EST279825
23	278.6	26.2	305	25	N65416	N65416 20456 Lambd
24	276	26.0	599	63	AM011134	AM011134 ST17B03 P
25	274	25.8	599	74	AM219797	AM219797 EST302279
26	268.8	25.3	304	36	T21150	T21150 3158 Lambda
27	265.4	25.0	637	80	AM350549	AM350549 GM210009A
28	264	24.8	465	45	A1352795	A1352795 MB61-10D
29	261.4	24.6	676	74	AM220075	AM220075 EST302558
30	257.6	24.2	430	79	AM307218	AM307218 sf54c07 Y
31	257.4	24.2	569	59	A1755448	A1755448 EST256548
32	253.4	23.8	428	42	A1100678	A1100678 33799 Lam
33	246	23.1	545	64	AM037836	AM037836 EST279465
34	244.2	23.0	337	20	Z34606	Z34606 ATTS3366 Ve
35	242.4	22.8	522	46	A1441759	A1441759 sa82d08 Y
36	237.8	22.4	667	74	AM185847	AM185847 se60d04 Y
37	235.2	22.1	541	64	AM036865	AM036865 614019G10
38	233.6	22.0	619	64	AM040482	AM040482 EST283442
39	233.8	21.9	612	47	A1496325	A1496325 sb05c09 Y
40	228.4	21.5	423	35	C22371	C22371 C22371 Rice
41	228.6	21.3	515	79	AM279515	AM279515 sf19e09 Y
42	226.8	21.2	570	50	A1676939	A1676939 605047A07
43	222.6	20.9	568	47	A1487272	A1487272 EST245594
44	221.4	20.8	616	42	AF074734	AF074734 AF074734
45	220.4	20.7	265	23	R84144	R84144 16103 Lambd

## ALIGNMENTS

RESULT 1  
LOCUS A1992868 469 bp mRNA  
DEFINITION 701493826 A. thaliana, Ohio State clone set Arabidopsis thaliana  
ACCESSION A1992868  
VERSION A1992868.1 GI:5839773  
KEYWORDS EST  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE 1 (bases 1 to 469)

AUTHORS

Chen J., Momiyama M., Chan E., Mooney M., Carroon B., Gilliland D., Wang X., Hillman J., Guejter K., Kim C., Doyle M., Brzoska P., Gorgone G., Burns D., Griffith J., Mounoutoua M., Nguyen D., Tan R., Rose M., Warren B., Ton B., Kastury K., Borillo C., Caprio T., Policky J., Suzuki G., Argentine C., Shah S., Nobrega A., Murry L., Turner C., Krikorian S., Elder L. and

TITLE Arabidopsis thaliana Gene Expression MicroArray  
JOURNAL Unpublished (1999)  
COMMENT On Dec 20, 1995 this sequence version replaced gi:1135328.  
Contact: David Smoller, Ph.D.  
Genome Systems, Inc., a wholly owned subsidiary of Incyte  
Pharmaceuticals, Inc.  
463 World Parkway Circle, St. Louis, MO 63134, USA  
Tel: 877-577-2733  
Fax: 314-427-3324  
Email: service@genomesystems.com.

FEATURES  
source location/Qualifiers  
1..469  
/organism="Arabidopsis thaliana"  
/db\_xref="taxon:3702"  
/clone="701493826"

BASE COUNT 120 a 124 c 89 g 136 t  
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Query Match 43.8% Score 465.8; DB 63; Length 469;  
Best Local Similarity 99.6%; Pred. No. 5.5e-108;  
Matches 467; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 1 acgaaccctaaatttgccttcctacatcttgatcagaaatattactaaattcattatgat 60  
QY 77 tactctcttcctacatcttcctacatcttcctacatcttcctacatcttcctacatcttc 136  
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DB 61 tactctcttcctacatcttcctacatcttcctacatcttcctacatcttcctacatcttc 120  
QY 137 tcgcagcttcctacatcttcctacatcttcctacatcttcctacatcttcctacatcttc 196  
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DB 121 tcgcagcttcctacatcttcctacatcttcctacatcttcctacatcttcctacatcttc 180  
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QY 257 ggaac 316  
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DB 241 ggaac 300  
QY 317 ggcctac 376  
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DB 301 ggcctac 360  
QY 377 ggaac 436  
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DB 361 ggaac 420  
QY 437 ctccgaac 485  
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DB 421 ctccgaac 469

RESULT 2

LOCUS R89998 556 bp mRNA

DEFINITION 16353 lambda-PRU2 Arabidopsis thaliana cdna clone 187H5T7, mRNA

ACCESSION R89998

VERSION R89998.1 GI:957538

KEYWORDS EST

SOURCE thale cress.

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;

REFERENCE 1 (bases 1 to 556)  
 AUTHORS Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomasnow,M., Retzel,E. and Somerville,C.  
 TITLE Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones  
 JOURNAL Plant Physiol. 106, 1241-1255 (1994)  
 MEDLINE 95148729  
 COMMENT On Apr 14, 1993 this sequence version replaced gi:693023.  
 CONTACT: Thomas Newman  
 MSU-DOE Plant Research Laboratory  
 Michigan State University  
 MSU-DOE-PR, Michigan State University, Plant Biology Bldg., E. Lansing, MI  
 Tel: 517-353-0854  
 Fax: 517-353-9168  
 Email: 22313cni@dm.cl.msu.edu  
 Seq primer: T7 dye primer.  
 FEATURES  
 source  
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 /organism="Arabidopsis thaliana"  
 /strain="var columbica"  
 /db\_xref="taxon:3702"  
 /clone="187H5T7"  
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 /note="Vector: lambda Zip-lox; Site.1: Sal; Site.2: Not; lambda PR2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRU's lambda Zip-lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dt primed cDNA."  
 BASE COUNT 151 a 118 c 123 g 146 t 18 others  
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 Best Local Similarity 94.4%; Pred. No. 4e-90;  
 Matches 441; Conservative 0; Mismatches 20; Indels 6; Gaps 3;  
 Oy 349 ctctctgacatcttgctgctgagcttggaaagcttgaacattacagatcagaagctc 408  
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 Db 1 CTCCTGACATCTTGGCGCTGAGCTTGGAGACTTGAACATTACATGATCTAGAGCTC 60  
 Oy 409 tacaaaaaacacatccaaagaaactataccttcgaaacttggaaactgaagaatctc 468  
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 Db 61 TACAAAAACAATCCAAAGAACATATACCTTCGAACTTGAATCTGAAGAATCTCATC 120  
 Oy 469 agcttgatctgtacaaacaaatctacagagatagttccactcttgggaaatg 528  
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 Db 121 AGCTTGATCTGTACAAACAACATCTTACAGGATGATGCCCTCTTGGGAAATTTG 180  
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 Db 181 AAGTCTCTGGCTTTTAAAGGCTTAATGACACCGATTGACGGGGCAATCCCTAGAGCA 240  
 Oy 589 ctcaactgcaatcccaagccttaaaagtgtgatgtctcaagcaatgattgtgtgaaaca 648  
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 Oy 649 atcccaacaacgagactttgtcaccatccttcaagaacttgaagaacaccgagag 708  
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 Db 301 ATCCCAACAACGAGACCTTTTGTCTCAATCTTTACAGAGACTTTGAGNACACCGAGG 360  
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 Db 361 TTGGNAGGAGACCGGAATTAATCTCGGTCTTGCACGCTNCGGCAATTAATGACCC--TGAAAA 417  
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Db 418 ATTGAAACCTGAAA--TGAGATTGGGGGTGNCCTTTAAGGCAC 462  
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 RESULT 3  
 LOCUS A1100481 442 bp mRNA EST 21-NOV-1998  
 DEFINITION 34856 Lambda-PR2 Arabidopsis thaliana cDNA clone 90J7XP 3', mRNA sequence.  
 ACCESSION A1100481  
 VERSION A1100481.1 GI:3450442  
 KEYWORDS EST.  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 REFERENCE 1 (bases 1 to 442)  
 AUTHORS Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomasnow,M., Retzel,E. and Somerville,C.  
 TITLE Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones  
 JOURNAL Plant Physiol. 106, 1241-1255 (1994)  
 MEDLINE 95148729  
 COMMENT On Jan 14, 1998 this sequence version replaced gi:1797474.  
 CONTACT: Thomas Newman  
 MSU-DOE Plant Research Laboratory  
 Michigan State University  
 MSU-DOE-PR, Michigan State University, Plant Biology Bldg., E. Lansing, MI  
 Tel: 517-353-0854  
 Fax: 517-353-9168  
 Email: 22313cni@dm.cl.msu.edu  
 The sequence entry for this EST has been reverse complimented and is being submitted in the sense orientation.  
 Seq primer: M13 Universal.  
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 /note="Vector: lambda Zip-lox; Site.1: Sal; Site.2: Not; lambda PR2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRU's lambda Zip-lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dt primed cDNA."  
 BASE COUNT 135 a 82 c 90 g 132 t 3 others  
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 Db 181 TGAAGAATTGGGGGAGTACCTTTAGAGAACACTTCACCACTTATCAAAATACACATCTA 240  
 QY 845 ctatgtataatgatatataatgagtcacaaataaataaagaatcgatcaatcat 904  
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 QY 1025 caagtgtctgtcctgtctgc 1046  
 Db 421 CAAGTTGTCTGCTGTCTGTCTGC 442

## RESULT 4

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 DEFINITION 33806 Lambda-PRL2 Arabidopsis thaliana cDNA clone 90J7XP 3', mRNA  
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 VERSION A1100685.1 GI:3449395  
 SOURCE EST.  
 ORGANISM thale cress.  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core  
 eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;  
 Arabidopsis.

REFERENCE 1 (bases 1 to 360)  
 AUTHORS Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.,  
 McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.,  
 Retzel,E. and Somerville,C.  
 TITLE Genes galore: a summary of methods for accessing results from  
 large-scale partial sequencing of anonymous Arabidopsis cDNA clones  
 Plant Physiol. 106, 1241-1255 (1994)  
 JOURNAL 95148729  
 MEDLINE  
 COMMENT On May 5, 1995 this sequence version replaced gi:797715.  
 Contact: Thomas Newman  
 MSU-DOE Plant Research Laboratory  
 Michigan State University  
 Lansing, MI  
 Tel: 517-353-0854  
 Fax: 517-353-9168  
 Email: 22313cnc@lhm.cl.msu.edu

FEATURES  
 source The sequence entry for this EST has been reverse complemented and  
 is being submitted in the sense orientation.  
 Seq primer: M13-21.  
 Location/Qualifiers

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 /organism="Arabidopsis thaliana"  
 /strain="var Columbia"  
 /db\_xref="taxon:3702"  
 /clone="90J7XP"  
 /clone\_1lb="lambda-PRL2"  
 /note="Vector: lambda Zip-Lox; Site\_1: Sal; Site\_2: Not;  
 Lambda PRL2 is a cDNA library derived from equal  
 quantities of 4 pools of mRNA. The mRNA sources were 1) 7  
 day germinated etiolated seedlings; 2) tissue culture  
 grown roots; 3) staged plants half with 24 hour light  
 cycle, half on 16 hr light, 8 hour dark- rosettes; 4)  
 same plants as 3 but aerial tissue (stems, flowers and  
 siliques. The vector is BRL's lambda Zip-Lox. The cDNA  
 inserts were directionally cloned with Sal-Not arms using

BASE COUNT 116 a 60 c 77 g 105 t 2 others  
 ORIGIN

Query Match 33.7%; Score 358; DB 42; Length 360;  
 Best Local Similarity 99.4%; Pred. No. 1.2e-80;  
 Matches 358; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 QY 867 tagtccaaaaaaatgaaagaatcgaaatcagtaatatcatctggtctcaattgagaact 926  
 Db 181 TAGTCCAAAAAATGAAAGATCGAATCAGTAAATATCACTGCTGCTGCAATTCAGAACT 240  
 QY 927 ttgaagttctgtgtatgtaaatcttaattcgaccttcggtactgtaattgttcgttg 986  
 Db 241 TTGAGGCTCTGTGTATGTAAATTTCTTAATCGCACTTTCGGCTGTATGTTCGGTTG 300  
 QY 987 tggattctcgagaagtaacattgttatgtgtatgtatcaagttgttcctgtctgc 1046  
 Db 301 TGGATNCTGAGAACTAATTTGTATGTATGTATGATCAAGTTGTTCTGCTGTCTGC 360

## RESULT 5

LOCUS A1100683 364 bp mRNA EST 21-AUG-1998  
 DEFINITION 33804 Lambda-PRL2 Arabidopsis thaliana cDNA clone 187H5XP 3', mRNA  
 ACCESSION A1100683  
 VERSION A1100683.1 GI:3449393  
 KEYWORDS EST.  
 SOURCE thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core  
 eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;  
 Arabidopsis.

REFERENCE 1 (bases 1 to 364)  
 AUTHORS Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.,  
 McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.,  
 Retzel,E. and Somerville,C.  
 TITLE Genes galore: a summary of methods for accessing results from  
 large-scale partial sequencing of anonymous Arabidopsis cDNA clones  
 Plant Physiol. 106, 1241-1255 (1994)  
 JOURNAL 95148729  
 MEDLINE  
 COMMENT On May 5, 1995 this sequence version replaced gi:797711.  
 Contact: Thomas Newman  
 MSU-DOE Plant Research Laboratory  
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 Email: 22313cnc@lhm.cl.msu.edu

FEATURES  
 source The sequence entry for this EST has been reverse complemented and  
 is being submitted in the sense orientation.  
 Seq primer: M13-21.  
 Location/Qualifiers

1..364  
 /organism="Arabidopsis thaliana"  
 /strain="var Columbia"  
 /db\_xref="taxon:3702"

/clone="187H5Xp"  
/note="Vector: lambda zip-lox; site\_1: Sal; site\_2: Not;  
lambda PRL2 is a cDNA library derived from equal  
quantities of 4 pools of mRNA. The mRNA sources were 1) 7  
day germinated etiolated seedlings; 2) tissue culture  
grown roots; 3) staged plants half with 24 hour light  
cycle, half on 16 hr light, 8 hour dark - rosettes; 4)  
same plants as 3 but aerial tissue (stems, flowers and  
siliques. The vector is BRU's lambda zip-lox. The cDNA  
inserts were directionally cloned with Sal-Not arms using  
oligo dt primed cDNA. " 2 others

BASE COUNT 113 a 80 c 70 g 99 t

ORIGIN

Query Match 32.9%; Score 349.4; DB 42; Length 364;  
Best Local Similarity 98.9%; Pred. No. 1.8e-78;  
Matches 361; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

OY 508 cccactcttgggaaatgaagctctctgcttcttaagcgttaatgaacacgattg 567  
|||||  
Db 1 CCCATTTCTTGGGAAATGCAAGCTTNT-GTCTTTTACGGCTTATGACAAACCGATTG 59  
OY 568 accgggccaatcccttagagcactctgcaatcccaagccttaagtgtgtatctca 627  
|||||  
Db 60 ACGGGGCCAATCCATGAGCCTCAGCCTCAATCCCAAGCCTTAAAGTGTGATGCTCA 119  
OY 628 agcaatgatgtgtggaacacatcccaacaaagacattgtctacattcttcaag 687  
|||||  
Db 120 AGCATATGATTTGTGTGAGAACATCCCAACAAAGGACCTTTGTCTCATCTTTTACAG 179  
OY 688 aacttgaagaacacccgaggttgagggagcgggaattactggtcttgcagactacgac 747  
|||||  
Db 180 AACTTTGAGAACACCCGAGGTTGAGGAGACCGGAATTAATCTCGCTCTTGAACCTAGAC 239  
OY 748 actactgcaactgcaaaatgtgcaaacctggaatgaagaattgggggtgacattg 807  
|||||  
Db 240 ACTTACTGCACTGAAAAAATGTGCAAAACCTGAAATGAGAAATTTGGGGGTGACCTTG 299  
OY 808 taagaacactaccactttatcaaatatcacacttactatgtatgaatataatgt 867  
|||||  
Db 300 TAAAGAACTTCAACCACTTATCAAAATATCACAATCTATGTAATATATATGT 359  
OY 868 agtcc 872  
|||||  
Db 360 AgTCC 364

RESULT 6  
AA394359 534 bp mRNA EST 30-OCT-1997  
LOCUS 25942 Lambda-PRL2 Arabidopsis thaliana cDNA clone 305G17 3', mRNA  
DEFINITION  
ACCESSION AA394359  
VERSION AA394359.1 GI:2047570  
KEYWORDS EST.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core  
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;  
Arabidopsis.  
1 (bases 1 to 534)  
Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.,  
McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomasow,M.,  
Retzel,E. and Somerville,C.  
Genes galore: a summary of methods for accessing results from  
large-scale partial sequencing of anonymous Arabidopsis cDNA clones  
JOURNAL Plant Physiol. 106, 1241-1255 (1994)  
MEDLINE 95148729  
COMMENT On May 18, 1995 this sequence version replaced gi:811121.  
Contact: Thomas Newman

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Fax: 517-353-9168  
Email: 22313c@ibm.cl.msu.edu  
Seq primer: 77.

FEATURES  
source Location/Qualifiers  
1..534  
/organism="Arabidopsis thaliana"  
/strain="var columbia"  
/db\_xref="taxon:3702"  
/clone="305G17"

/note="Vector: lambda zip-lox; site\_1: Sal; site\_2: Not;  
lambda PRL2 is a cDNA library derived from equal  
quantities of 4 pools of mRNA. The mRNA sources were 1) 7  
day germinated etiolated seedlings; 2) tissue culture  
grown roots; 3) staged plants half with 24 hour light  
cycle, half on 16 hr light, 8 hour dark - rosettes; 4)  
same plants as 3 but aerial tissue (stems, flowers and  
siliques. The vector is BRU's lambda zip-lox. The cDNA  
inserts were directionally cloned with Sal-Not arms using  
oligo dt primed cDNA. " 18 others

BASE COUNT 151 a 114 c 125 g 126 t

ORIGIN

Query Match 31.7%; Score 336.8; DB 33; Length 534;  
Best Local Similarity 85.1%; Pred. No. 2.8e-75;  
Matches 404; Conservative 0; Mismatches 62; Indels 9; Gaps 3;

OY 467 tcaagtgtatctgtacacaaactctacagggatagttccactcttgggaaat 526  
|||||  
Db 1 TCAGCTTGATCTGTACAAACAACTTACAGGATAGTCCCACTCTTGGGAAAT 60  
OY 527 tgaatctctgtcttcttaagcgttaatgaacacgattgaaggggccaatccctagag 586  
|||||  
Db 61 TGAAGCTTGTGCTTTTATGCGCTTAATGACAAACGATGACCGTCAATCCCTTAG 120  
OY 587 caactcactcaatcccaagccttaagtgtgtatgtctcaagaatgattgtgaa 646  
|||||  
Db 121 CACTACGGCAATCCCAAGCCTTAAAGTTGTGACGTCTCAAGCAATATTTGTGTGAA 180  
OY 647 caatcccaacaaagacatttgcacatcccttaagaacttgaagaacaccca 706  
|||||  
Db 181 CAATCCCAACAAACGACCTTTGCTCAATCTCTTACAGAACTTGAGAAACCCGA 240  
OY 707 ggttggagggacgggaattactcgtcttgcagatgaagaactaacgcctgaaaaa 766  
|||||  
Db 241 GATTGGAGGACCGGAATTAATCTGCTTTCGAAAGCTAGACATCACTGAGNACGAAACA 300  
OY 767 atggcaaaccttgaagaattggggggtg---acctgtaagaacattcacca 823  
|||||  
Db 301 ACTGGCAAAACCTGGAATGAGNATTTGGGGGGGTGACCTTTGAAGNACACTTCNCA 360  
OY 824 cttaacaatacacatctac---tatgtaataagatatatatgtatccaaa---aa 877  
|||||  
Db 361 CATTATCCAAATATCCACATCCATTANGNATNATGATATATGNGGTAAACCAA 420  
OY 878 aaaaatgaagaatgaatcaatgataatcatatcgtctcaattggaacttggag 932  
|||||  
Db 421 AAAAATTGGGGATCCGATCGGAGANANACGGGCCCAATTTGGGAATGNGGG 475

RESULT 7  
A1100682 348 bp mRNA EST 21-AUG-1998  
LOCUS 33803 Lambda-PRL2 Arabidopsis thaliana cDNA clone 105L1XP 3', mRNA  
DEFINITION  
ACCESSION A1100682  
VERSION A1100682.1 GI:3449392

KEYWORDS	EST.
SOURCE	thale cress.
ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
AUTHORS	1 (bases 1 to 348) Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhe,N., Somerville,S., Thomasrow,M., Retzel,E. and Somerville,C.
TITLE	Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones
JOURNAL	Plant Physiol. 106, 1241-1255 (1994)
MEDLINE	95148729
COMMENT	On May 5, 1995 this sequence version replaced gi:797667. Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan State University MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, MI Tel: 517-353-0854 Fax: 517-353-9168 Email: 22313c@edbm.cl.msu.edu The sequence entry for this EST has been reverse complimented and is being submitted in the sense orientation. Seq primer: M13-21.
FEATURES	Location/Qualifiers 1..348 /organism="Arabidopsis thaliana" /strain="var columbia" /db_xref="taxon:3702" /clone="1B5L1XP" /clone_lib="lambda-PRL2" /note="Vector: lambda zip-lox; Site_1: Sal; Site_2: Not; lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) straged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques). The vector is BRU's lambda zip-lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dt primed cDNA."
BASE COUNT	110 a 74 c 66 g 93 t 5 others
ORIGIN	
Query Match	31.2%; Score 332; DB 42; Length 348;
Best Local Similarity	99.1%; Pred. No. 4, 5e-74;
Matches 332; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	
OY	538 gtccttttaaggcttaatgaacaacccgattacggggccaatccctagagcactcgtca 597 
Db	14 gtccttttaaggccttaaaagacaaacgattgacggggccatcmttagagcactcgtca 73 
OY	598 atcccaagccttaaaagttgttgatgltctcaagaacatgattgtgtggaacaatcccaaca 657 
Db	74 atcccaagccttaaaagttgttgatgltctcaagaacatgattgtgtggaacaatcccaaca 133 
OY	658 aacggaccttctgcacatctcctttacaagaaccttggagaacaaccgaggttggaggg 717 
Db	134 AACGAGACCTTTTGGTCACATTCCTTTACGAGACTTTGAGAAACACCCGAGGTGGAGGGA 193 
OY	718 ccgggaataactcgtgcttcgcaagcttaagacataactgacactgagaanaaatgtggcaaac 777 
Db	194 CCGGATTAATCTGNCCTTGCACAGCTACGACACTTAATCTGCAGAAAAAATTGGGAAAAAC 253 
OY	778 ctgaanaatgaagaacttgggggttgacctgtgaagaacaacttaccacacttaacaatatc 837 
Db	254 CTGAAATGAACAATTTGGGGGCTGANCCTTGTAAGAACAACCTTACCACCTTATCAATAATAC 313 
OY	838 acatctactatgtlaataaglatatataatgtagtgc 872

Db	314	ACATCTACTAGTATATAAGTAGTATATATAGTAGTC	348
(     )			
RESULT	8		
LOCUS	AA712221	401 bp mRNA	EST
DEFINITION	31949 lambda-PRL2 Arabidopsis thaliana cDNA clone 180C977,		24-DEC-1997
ACCESSION	AA712221		
VERSION	AA712221.1	GI:2722138	
KEYWORDS	EST.		
SOURCE	thale cress.		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS	euphyllipytes; Spermatophyta; Magnoliophyta; eudicotyledons; core		
TITLE	eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;		
JOURNAL	Arabidopsis		
MEDLINE	1 (bases 1 to 401)		
COMMENT	Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomasow,M., Retzel,E. and Somerville,C. Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones plant Physiol. 106, 1241-1255 (1994) On Sep 19, 1997 this sequence version replaced gi:1520373. Contact: Thomas Newman MSU-DOE Plant Research Laboratory Michigan State University MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, MI Tel: 517-353-0854 Fax: 517-353-9158 Email: 22313cne@dm.cl.msu.edu Seg primer: T7 dye primer. Location/Qualifiers 1..401 /organism="Arabidopsis thaliana" /strain="var columbia" /db_xref="taxon:3702" /clone="180C977" /note="Vector: lambda ZAP-Lox; Site_1: Sal; Site_2: Not; lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques). The vector is BRV's lambda ZAP-Lox. The cDNA inserts were directionally cloned with Sal-not arms using oligo dt primed cDNA."		
FEATURES	source		
BASE COUNT	103 a 105 c 78 g 99 t 16 others		
ORIGIN			
Query Match	31.0%, Score 329.2; DB 37; Length 401;		
Best Local Similarity	89.8%; Pred. No. 2.3e+73;		
Matches 354; Conservative 0; Mismatches 39; Indels 1; Gaps 1;			
Db	85 ctgcagctcgatggccacatggcgtctgaacctgagtggagactcttcgaact 144		
	1 CTTAAACNCGAANGCTCACATGCGCTCTCAAACTATCGGTGGAGACTCTTCGA 60		
0y	145 tcgttaatcctaacttagcttgattcaactgctgcgaagaacctccgaaggagatgct 204		
Db	61 TCGTTAACCCCTTAAGCTTTATTATACCGNGCTGCAAGAACAACGCCAAGNANTNCT 120		
0y	205 ctttgcgtcttcggcggagtttaacaatcgcgaccatgtcttcagaagcttgatacca 264		
Db	121 CTCATAGGCTCTTGCGGAGATTGCACAGATCCAGACCATGTCTCTCAAGACTGGATCCA 180		



QY	265	acctgttcaatccctgtacacccgtgtccatcttcaacctgttcaacaagaacccgtccat	324
Db	181	ACINTHTSTNAATCCTTGTAACCGTTCCTCATGTNACCTCTTAACCAAGACACCCGTCAC	240
QY	325	ctgtgtgatttggggatccaacacctctctgagacatcttgcgcttgagcttgggaacct	384
Db	241	CGTGTGATTTGGGAATTTCAAAACNNCTCTGGACATCTTGCGNCTGAGCTTGGGAAGCTT	300
QY	385	gaacatttcagatctagaagctctcaaaaacaacccaagaagacttaaccttcgaa	444
Db	301	GAACATTTCAGATCTAGAAGCTCTTACAAAACCAACCATCAAGACTATACCTCCGAA	360
QY	445	cttggaaattcgaagatctcatcagcttggatc	478
Db	361	CTTGGAAATCTGAAG-ATCTCATCAAGNTTGGATC	393
RESULT	9		
LOCUS	H37300	353 bp	MRNA
DEFINITION	15429 Lambda-PRL2 Arabidopsis thaliana cDNA clone 179J1977, mRNA sequence.		EST
ACCESSION	H37300		30-DEC-1997
VERSION	H37300.1	GI:906799	
KEYWORDS	EST.		
SOURCE	thale cress.		
ORGANISM	Arabidopsis thaliana		
REFERENCE	1 (bases 1 to 353)		
AUTHORS	Newman,T., deBrujn,F.J., Green,P., Keegstra,K., Kende,H., McInosh,L., Ohlroge,D., Ratkbel,N., Somerville,S., Thomasow,M., Retzel,E. and Somerville,C.		
TITLE	Gene glorie: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones		
JOURNAL	Plant Physiol.	106,	1241-1255 (1994)
MEDLINE	95146729		
COMMENT	On May 8, 1995 this sequence version replaced g1:801146.		
	Contact: Thomas Newman		
	MSU-DOE Plant Research Laboratory		
	Michigan State University		
	MSU-DOE-PR, Michigan State University, Plant Biology Bldg., E.		
	I Lansing, MI		
	Tel: 517-353-0854		
	Fax: 517-353-9168		
	Email: 223j3t@edlm.c1.msu.edu		
	Seq primer: T7 dye primer.		
FEATURES	Location/Qualifiers		
source	1..353		
	/organism="Arabidopsis thaliana"		
	/strain="var columbia"		
	/db_xref="taxon:3702"		
	/clone="179J197"		
	/clone.lib="lambda-PRL2"		
	/note="Vector: lambda zip-lox. site.1: Sal; site.2: Not; Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda zip-lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dt primed cDNA."		
BASE COUNT	98 a	85 c	67 g 89 t 14 others
ORIGIN			
Query Match	30.8%	Score 327.8;	DB 23; Length 353;
Best Local Similarity	94.1%;	Pred. No. 5.2e-73;	
Matches 333; Conservative	0;	Mismatches 21;	Indels 0; Gaps 0;

	DB	1	TACAAAACAATCCAGAGAACTTACTTCGCAACTTGGAATTCGAAGATTCATC	60
OY	469	aagcttgatcgtacaaacaactctaacaggatagttcccaacctcttgggaaaattg	528	
DB	61	AGCTGGTTCTGTACAMACMANOTWTACAGAGVWAGTCCACTTNTTGGGAAAAATTG	120	
OY	529	aagtcctcgatcctttaagcgttaataaacaccgataggccggggccaatcccctaataga	588	
DB	121	ANGTCTCTGTGCTTTTNACGCCTTAATACACCAGATTGACCGGTCCAATCCTTAGNCA	180	
OY	589	ctcacgtgaatcccccaagccttaaagtgtgtatgtlcttaagaatgatttgttggtaaca	648	
DB	181	CTCACGGCAATCCCAAGCNTWTAAGTTGTGANCTCANCANATGATTTGTGTGANA	240	
OY	649	atccccaaaaagcgacctttgtctaaccttcctttaagaactttggaaacacccggag	708	
DB	241	ATCCCAACAAACAGGAGCCCTTCTCTACATTCCTTTACAGAATCTTGAGAACACCCGNGA	300	
OY	709	ttagaggaacgggaattactcgtgtcttgcaagctacgacctaactgcgcctg	761	
DB	301	JTGAGAGGNCCGANTTACTCGTCTTGCAAGNTACGGCACTAATCATNCCTG	353	
RESULT	10			
	AW43205			
LOCUS	AW43205	608 bp	mRNA	EST
DEFINITION	EST308135 tomato mixed elicitor, BRI Lycopersicon esculentum cDNA			17-FEB-2000
ACCESSION	AW43205			
VERSION	AW43205.1	GI:6985387		
KEYWORDS	EST.			
SOURCE	tomato.			
ORGANISM	Lycopersicon esculentum			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	euphylliphtes; Spermatophyta; Magnoliophyta; eudicotyledons; core			
	eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;			
	Lycopersicon.			
REFERENCE	1 (bases 1 to 608)			
AUTHORS	D'Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Hansen,T.S., Rohning,C.M., Craven,M.B., Bowman,C.L., Nierman,M., Fraser,C.M., Venter,J.C., Tanksley,S.D., Giovannoni,J.J. and Martin,G.B. Generation of ESTs from tomato callus (mixed elicitor) Unpublished (1999) On Dec 20, 1995 this sequence version replaced gi:1133853. Contact: David Frisch Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 4366 Fax: 864 656 4293 Email: dfrisch@CLEMSON.EDU			
TITLE				
JOURNAL				
COMMENT				
FEATURES				
Source				
	Location/Qualifiers			
	1..608			
	/organism="Lycopersicon esculentum"			
	/cultivar="Rio Grande Flor"			
	/db_xref="taxon:4081"			
	/clone="CLEF43M10"			
	/clone.lib="tomato mixed elicitor, BRI"			
	/tissue_type="leaf"			
	/dev_stage="4-6 week old plants"			
	/lab_host="XL1-Blue MR"			
	/note="Vector: pBluescript SK(-); site_1: EcoRI, site_2: XhoI; CLEF - Inoculated with a variety of disease response elicitors. Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenthion, ETX, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."			
PAGE COUNT	165 a	126 c	134 g	183 t



Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; eumphylophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 339)  
 Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel,E. and Somerville,C.  
 Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)  
 95148729  
 On May 5, 1995 this sequence version replaced gi:797664.  
 Contact: Thomas Newman  
 MSU-DOE Plant Research Laboratory  
 Michigan State University  
 MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, MI  
 Tel: 517-353-0854  
 Fax: 517-353-9168  
 Email: 22313tcm@lhm.cl.msu.edu  
 The sequence entry for this EST has been reverse complemented and is being submitted in the sense orientation.  
 Seq primer: M13-21.

FEATURES  
 source  
 1..339  
 /organism="Arabidopsis thaliana"  
 /strain="var columbia"  
 /db\_xref="taxon:3702"  
 /clone="179J11XP"  
 /note="Vector: lambda Zip-lox; Site\_1: Sal; Site\_2: Not; lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA."

BASE COUNT 104 a 75 c 66 g 89 t 5 others  
 ORIGIN

Query Match 29.6%; Score 314.6; DB 42; Length 339;  
 Best Local Similarity 97.0%; Pred. No. 1.2e-69;  
 Matches 328; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 536 tggctcttttcaggttcataacacacgattgacggggccaa-tccctagagcactact 594  
 |||  
 DB 2 tggctcttttcaggttcataacacacgattgacggggccaa-tccctagagcactact 61

QY 595 gcaatcccaagccttaagtgatgtctcaagcaatgtttgtggaacaatccca 654  
 |||  
 DB 62 gcaatcccaagccttaagtgatgtctcaagcaatgtttgtggaacaatccca 121

QY 655 acaaacgagcctttgtctacatctccttaacagaaattggaacaacccgagttgag 714  
 |||  
 DB 122 ACAAAAGGAGCTTTTGTCACATCTCTTACAGAACTTTGGAACAACCCGAGTTGAG 181

QY 715 ggaacggaattactcgttcgttgaagtaagcaactaacctgacactgaaaaattggca 774  
 |||  
 DB 182 GGACCGGAATTACTCGGGGTGCAAGCTACGACACTACCTGCAAAAATTGGGCA 241

QY 775 aacctgaaaaaagaattgggggtggaacctgtgaagaacacttaccacttacaat 834  
 |||  
 DB 242 AANCTGAAAATAGAGAAATTGGGGGTGACCTTGTAAGAACCTTACCACTTTAGCAAT 301

QY 835 atcacatctactatgtaataagtatatatatgtagtc 872  
 |||  
 DB 302 ANCACATCTACTATGTAAATATATATATGTAGNCC 339

RESULT 13  
 H36800 447 bp mRNA EST 30-DEC-1997  
 LOCUS  
 DEFINITION 14929 Lambda-PRL2 Arabidopsis thaliana cDNA clone I79A2277, mRNA sequence.  
 ACCESSION H36800  
 VERSION H36800.1 GI:906299  
 KEYWORDS EST.  
 SOURCE Thale cress.  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; eumphylophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
 1 (bases 1 to 447)  
 Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M., Retzel,E. and Somerville,C.  
 Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)  
 95148729  
 Contact: Thomas Newman  
 MSU-DOE Plant Research Laboratory  
 Michigan State University  
 MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, MI  
 Tel: 517-353-0854  
 Fax: 517-353-9168  
 Email: 22313tcm@lhm.cl.msu.edu  
 Seq primer: T7 dye primer.

FEATURES  
 source  
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 /organism="Arabidopsis thaliana"  
 /strain="var columbia"  
 /db\_xref="taxon:3702"  
 /clone="179A2277"  
 /note="Vector: lambda Zip-lox; Site\_1: Sal; Site\_2: Not; lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA."

BASE COUNT 106 a 115 c 83 g 126 t 17 others  
 ORIGIN

Query Match 28.4%; Score 302.4; DB 23; Length 447;  
 Best Local Similarity 86.9%; Pred. No. 1.5e-66;  
 Matches 371; Conservative 0; Mismatches 43; Indels 13; Gaps 4;

QY 14 ccgagaaacccaatttgccttcctcattc-tgttcagaanaatt-----actca 62  
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 DB 22 CCAACGTAACCCCTTAATTTCCTCTCTCTGTCAGAAAATTTCCCTTACNCTCA 81

QY 63 aatccctattagatactctctcttggaactcogatagcctcaatgagctctgaaacta 122  
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 DB 82 AATTCCTTTTGATGATTCCTCTCTTAACCCGAAAGCTCACATGGCGTCTGAAACTA 141

QY 123 tcggttggaagctctcgacagcttgtaaccttaaccttagcttgtaacctggtcga 182  
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 DB 142 TCGGTGGAGCTCTTCCAGCTTGTTAACTTACCTTACCTTACCTTACCTTACCTTAC 201

QY 183 agcaaacctcgaagagatgctcttaagctcttcgcggagtttaacagacagcagca 242  
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 DB 202 AGCAAACTCCGAAGA-NTGCTCTCTACGCTCTTCGCGGAGTTTGACAGATCCAGACCA 260













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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,891A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02370-058910US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5992 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(512..3149, 3993..4393)
OTHER INFORMATION: /product= "RRK-B"
OTHER INFORMATION: /note= "Xa21 Xanthomonas spp. disease
OTHER INFORMATION: resistance gene RRR-B from rice (Oryza
US-08-475-891A-3
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Query Match          6.0%; Score 63.6; DB 3; Length 5992;
Best Local Similarity 50.3%; Pred. No. 6.7e-10;
Matches 156; Conservative 0; Mismatches 154; Indels 0; Gaps 0;
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QY 346 aacctctctggaacatcttgccgctgagcttgggaagcttgaacattacagatctagag 405
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DB 1670 AAGTTCACAGAGAGCAATCCGAGGATATGCGCAATCTTATTTGGCTTACACATCTCTAT 1729

QY 406 ctctcaaaaacaacatccaaggaactatctccgaacttgaacttgaagaattcc 465
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1730 CTCTGCAACACAAATTTCAAGGCTCTCTTCATCATCGTTGAGGCGAGCTTAATAAATTA 1789

QY 466 atcagcttgatctgtacaacaacatctacagggatagttcccactcttgggaaaa 525
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1790 GGCAATCTACTCGGCTACGAAACAACTTGAGCGGTTGATCCCGTTGGGCATAGGAAT 1849

QY 526 ttgaagctctgtgctctttaaagcttaataagacaacgatgacgggccaatccctaa 585
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1850 CTTACTGAACTTAAATATCTTACTGCTGCGACACAAATTCAGTGGTTGGATACCATAC 1909

QY 586 gcaactacatcccaagccttaagttgtgaagctcaagcctgaagatattgtgtga 645
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1910 ACACCTCAACACCTCAACAACTTGTTGTCTATTAGGCTTTCAACTAATACCTTAATGCT 1969

QY 646 acaatcccaa 655
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DB 1970 CCAATACCCA 1979
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RESULT 4
US-08-238-163-3
; Sequence 3, Application US/08238163
; Patent No. 5569830
; GENERAL INFORMATION:
; APPLICANT: BENNETT, Alan
; APPLICANT: LABAVITCH, John M.
; APPLICANT: POWELL, Ann
; APPLICANT: STOLTZ, Henrik
```

```

TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL
TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEASE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/238,163
FILING DATE: 03-MAY-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 2307E-540
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2075 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 421..1401
US-08-238-163-3
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Query Match          5.5%; Score 58; DB 1; Length 2075;
Best Local Similarity 50.5%; Pred. No. 2e-08;
Matches 196; Conservative 0; Mismatches 185; Indels 7; Gaps 2;
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QY 269 ttgttaatcccttgaacctggttgcattgtaacctgttaaccaagaacacggatcgtg 328
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DB 576 TTGCTGTTACTGTAAGTATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 631

QY 329 tggatttgggaattcaaacctctctggaactcttgccgctgagcttgggaagctgaac 388
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DB 632 TCACCGTCTTCCAGCAAGCAATATCTCGGCGCAAAATTCGCGCAGCGGTGAGACCTTCAT 691

QY 389 attacagatctagagctctacaaa---aaacaacatccaaggaactataactctcgaac 445
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 692 ATCTCGAATACTTGAATTTTCATATCTTACTATCTACCTGACGGAACAATTCACCTGCAA 751

QY 446 ttggaactctaaagatctcaacagcttgatctgtacaacaacaactcttaagggatag 505
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 752 TTGGGAAGCTCACAAACTTCAAAATGTTAAGGCTCAAGCTTCACTAATACCTTACAGGTCGA 811

QY 506 ttcccaactcttgggaanaattgaagctctgtgctctttaaagcttaatgacaacgat 565
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 812 TCCCTGAATTCCTTACTAGCTAGCTGAGGAATTTGACGTTGCTGAGATTGAATTAACAATCAAT 871

QY 566 tgacggggccaatccctagagcaactacatgcaatcccaagccttaagttgtatgct 625
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DB 872 TTACCGGAACAATCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 931

QY 626 caagcaatgatattgttgaacaatccc 653
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DB 932 ATCGTAACAACTCACCGGAACAATACC 959
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RESULT 5
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1648..4383, 5178..5513)
; OTHER INFORMATION: /product= "RRK-F"
; OTHER INFORMATION: /note= "Xa21 Xanthomonas spp. disease
; OTHER INFORMATION: resistance gene RRK-F from rice
; OTHER INFORMATION: (Oryza sativa)"
US-08-567-375-1

Query Match          5.2%; Score 55.4; DB 4; Length 6256;
Best Local Similarity 50.2%; Pred. No. 2.4e-07;
Matches 165; Conservative 0; Mismatches 161; Indels 3; Gaps 1;

QY 329 tggatttgggaattcaaacctctctgacacattgagccttgaggagcttgagac 388
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QY 389 att---taacagatctaagctctacaacaaacatcccaaggagactatcctccgaac 445
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DB 2795 CTTCGCTTAGTTTCTTGCACCTTGATTGAAATAGATACAGAGACATTCCTCAAGGATA 2854

QY 446 ttggaatctgaagaatctcatcagcttgatctgtacaacaacatctacaggagatag 505
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DB 2855 TTGGCAATCTTATTGGCTTACAAACATCTCTATCTCTGCAACACAAATTTCAGAGGCTCAC 2914

QY 506 ttcccaactcttgggaaatgaagtcctcgtctcttttaccggttaatgacaacggat 565
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DB 2915 TTCCATCATCTGTTGGGCGAGCTTAGAAMAATTAGGCATTCTAGTCCCTACACAAAACAAC 2974

QY 566 tgaaggggccaatccctagagcactcagcactcgaatcccaagcttaagttgtatgctc 625
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DB 2975 TGAGCGGTTTCATTCCTCATTCCTGATGGCCATAGCAAACTTACTGAACTTAATCTTACTGCTCG 3034

QY 626 caagcaatgatctgtgtggaacaatccca 654
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DB 3035 GCACCAACAATTCAGTGTGATGATACCA 3063

RESULT 9
; Sequence 1, Application US/08587680A
; Patent No. 5977434
; GENERAL INFORMATION:
; APPLICANT: Ronald, Pamela C.
; APPLICANT: Wang, Guo-Liang
; APPLICANT: Song, Wen-Yuang
; APPLICANT: Szabo, Veronique
; TITLE OF INVENTION: Procedures and Materials for Conferring
; TITLE OF INVENTION: Disease Resistance in Plants
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/587,680A
; FILING DATE: 17-JAN-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,375
; FILING DATE: 17-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/475,891
; FILING DATE: 07-JUN-1995
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/004,645
; FILING DATE: 29-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/567,375
; FILING DATE: 04-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-0589400S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6256 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1648..4383, 5178..5513)
; OTHER INFORMATION: /product= "RRK-F"
; OTHER INFORMATION: /note= "Xa21 Xanthomonas spp. disease
; OTHER INFORMATION: resistance gene RRK-F from rice (Oryza
; OTHER INFORMATION: sativa)"
US-08-587-680A-1

Query Match          5.2%; Score 55.4; DB 4; Length 6256;
Best Local Similarity 50.2%; Pred. No. 2.4e-07;
Matches 165; Conservative 0; Mismatches 161; Indels 3; Gaps 1;

QY 329 tggatttggggaattcaaacctctctgacacattgagccttgaggagcttgagac 388
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QY 389 att---taacagatctaagctctacaacaaacatcccaaggagactatcctccgaac 445
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DB 2795 CTTCGCTTAGTTTCTTGCACCTTGATTGAAATAGATACAGAGACATTCCTCAAGGATA 2854

QY 446 ttggaatctgaagaatctcatcagcttgatctgtacaacaacatctacaggagatag 505
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DB 2855 TTGGCAATCTTATTGGCTTACAAACATCTCTATCTCTGCAACACAAATTTCAGAGGCTCAC 2914

QY 506 ttcccaactcttgggaaatgaagtcctcgtctcttttaccggttaatgacaacggat 565
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DB 2915 TTCCATCATCTGTTGGGCGAGCTTAGAAMAATTAGGCATTCTAGTCCCTACACAAAACAAC 2974

QY 566 tgaaggggccaatccctagagcactcagcactcgaatcccaagcttaagttgtatgctc 625
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DB 2975 TGAGCGGTTTCATTCCTCATTCCTGATGGCCATAGCAAACTTACTGAACTTAATCTTACTGCTCG 3034

QY 626 caagcaatgatctgtgtggaacaatccca 654
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DB 3035 GCACCAACAATTCAGTGTGATGATACCA 3063

RESULT 10
; Sequence 1, Application US/08473553A
; Patent No. 5859338
; GENERAL INFORMATION:
; APPLICANT: Meyerowitz, Elliot M.
; APPLICANT: Clark, Steven E.
; APPLICANT: Williams, Robert W.
; TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
; TITLE OF INVENTION: Transformed Plants, and Proteins
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Honbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
```

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; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/473,553A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Silva, Robin M.
; REGISTRATION NUMBER: 38,304
; REFERENCE/DOCKET NUMBER: A-60886/RET/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5733 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2434..5037
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 5117..5467
; US-08-473-553A-1
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Query Match          5.0%; Score 53; DB 3; Length 5733;
Best Local Similarity 50.6%; Pred. No. 1.3e-06;
Matches 128; Conservative 0; Mismatches 125; Indels 0; Gaps 0;
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QY 408 ctacaaacacacatccaggaactatcctccgaacttggaaatctgaaagatcctat 467
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DB 3120 CTACGTACACACACTACACCGGTGGTGTCCACGCGAGTTCGGTGTAAACAACCTTGA 3179
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QY 468 cagcttgatctgtacaaacacacatccttaagagatagttcccaactcttgggaaatt 527
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DB 3180 GATCCTCGACATGGCGAGCTGTACACTCACCGAGAGATTCGACGAGTTAAAGTAACT 3239
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QY 528 gaagtcctgctctttttagcgcttaataagcgaattgaagggccaatccctagagc 587
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DB 3240 GAAACATCTACATACCTCTTCTTCACATCAACAACCTTACCGGTCAATATCCACCGGA 3299
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QY 588 actcactgcaatcccaagccttaagttgtgtagtctcgaagcaatgattgtgtggaac 647
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DB 3300 GCTTTCGGTGTAGTACGCTTGAATCTCTCGATTATCAATCAATCAATGTAACCGGAGA 3359
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QY 648 aatcccaacaac 660
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DB 3360 AATCCTCAAGC 3372
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RESULT 11
US-08-567-375-15
; Sequence 15, Application US/08567375
; Patent No. 5952485
; GENERAL INFORMATION:
; APPLICANT: Ronald, Pamela C.
; APPLICANT: Wang, Guo-Yuang
; APPLICANT: Song, Wen-Yuang
; APPLICANT: Szabo, Veronique
; TITLE OF INVENTION: Procedures and Materials for Confering
; TITLE OF INVENTION: Disease Resistance in Plants
```

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; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/567,375
; FILING DATE: 04-DEC-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/004,645
; FILING DATE: 29-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/475,891
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/373,375
; FILING DATE: 17-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-058930
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-567-375-15
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Query Match          4.8%; Score 50.8; DB 4; Length 831;
Best Local Similarity 48.6%; Pred. No. 2.1e-06;
Matches 139; Conservative 0; Mismatches 147; Indels 0; Gaps 0;
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QY 353 ctgagacatcttgccctgagcttgggaagcttgaacattacagtactlagagcttaca 412
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DB 33 CTGCTGACACTTCCTAGTGTGTTGGAAACTATTCAGGCTGAGAAATCTGTGTAACTG 92
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QY 413 aaacacacatcccaaggaactatcctccgaacttggaaatctgaaagatcctatagct 472
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 93 GAAATGGTCTCTCGATGATATCCCTCTGATATGCGACACTAAAGACATCTTAAAC 152
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QY 473 tggactgtacaaacacacatccttacaaggaagttcccaactcttgggaaattgaagt 532
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DB 153 TGGACTCGAGTAGAAGAACTCTCTGCGACATCCCTCTCGATTTGTAATGTCTTT 212
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 533 ctctgtctcttttagcgcttaatgacaacccgaattgaagggccaatccctagagcactca 592
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DB 213 CCTTAACCTACTTGATTTGAGCCAAATCAACTTCTGTGCTTATCCAGTCAATTTG 272
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 593 ctgcaatcccaagccttaagttgtgtagtctcgaagcaatgatt 638
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DB 273 CTCAATTCACATCTTAAATTAATCAATATTTCTGGAATCACTT 318
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RESULT 12
US-08-666-271-4
; Sequence 4, Application US/08666271
; Patent No. 5920000
; GENERAL INFORMATION:
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Db 2973 TGGAGCTTCGATGCTGATGCTGCTCAAGTCTTGAAGGTCATATACCGGATCATTT 3032  
QY 519 gggaaatgaagctctgctgtcttttaagcgttaagacaacccgattgagggccaat 578  
Db 3033 TCAGAAATTATACAGTACGATCGAATCTTTGGAATCTCTCATCTAATTAATCAGCGAGAAAT 3092  
QY 579 ccctaagagcactcactgcaatcccaagccttaagttgttgatgctcaagcaatgattt 638  
Db 3093 TCCCGACGACGCTTCGATCCCTCACATTCCTTGAAGTCTTAATCTCTCCACATCATCTT 3152  
QY 639 gtgtggaacaatcccaacaacgagcctttgct 672  
Db 3153 TGTGTGATGATCCCAAGAAACAATTTGAT 3186

RESULT 14  
US-08-244-646-14  
; Sequence 14, Application US/08244646  
; Patent No. 5744692  
; GENERAL INFORMATION:  
; APPLICANT: Cervone, Felice  
; APPLICANT: De Lorenzo, Giulia  
; APPLICANT: Salvi, Giovanni  
; APPLICANT: Albersheim, Peter  
; APPLICANT: Darvill, Alan  
; APPLICANT: Bergmann, Carl  
; TITLE OF INVENTION: Nucleotide Sequences Coding An  
; TITLE OF INVENTION: Endopolygalacturonase Inhibitor  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sally A. Sullivan  
; STREET: 5370 Manhattan Circle Suite 201  
; CITY: Boulder  
; STATE: CO  
; COUNTRY: US  
; ZIP: 80303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/244,646  
; FILING DATE: 06-JUN-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IT RM 91A 000915  
; FILING DATE: 06-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/IT/00158  
; FILING DATE: 04-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sullivan, Sally A.  
; REGISTRATION NUMBER: 32,064  
; REFERENCE/DOCKET NUMBER: 19-94  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303)499-8080  
; TELEFAX: (303)499-8089  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1116 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Phaseolus vulgaris  
; STRAIN: Saxa  
; IMMEDIATE SOURCE:  
; CLONE: lambda PGIP-3.3

FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1026  
; FEATURE:  
; NAME/KEY: 3'UTR  
; LOCATION: 1027..1116  
US-08-244-646-14

Query Match 3.9%; Score 41.4; DB 2; Length 1116;  
Best Local Similarity 48.1%; Pred. No. 0.0021;  
Matches 117; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 411 caaaacaacatccaaggaactatactccgaacttggaaatctgaagatctcatag 470  
Db 342 CATCAATACCTCGTCGGTCCATCCCGCCCATCGCTTAACCTCACCCACATCCCACTA 401  
QY 471 ctgtgatctgtacaacaatcttacagggatagttcccaactcttgggaaatgaa 530  
Db 402 TCTCTATATACACTCACACCAATGTCTCCGGCGCANATACCGATTCTTGTACAGATCA 461  
QY 531 gtcctgtgtcttttaagcgttaatgaacaacgattgaagggccaatccctagagact 590  
Db 462 AACCTCGTACCCCTCGACTTCTCCTACACAGCCCTCTCCGACACCTCCCTCCCTCAT 521  
QY 591 cactgcaatcccaagccttaagttgttgatgctcaagcaatgattgtgtgaaat 650  
Db 522 GCTTCTCTCCCAACGTCGGAGATCAATCGACGGCAACCGAAATCTCGGCGCAT 581  
QY 651 ccc 653  
Db 582 CCC 584

RESULT 15  
US-08-592-936B-20  
; Sequence 20, Application US/08592936B  
; Patent No. 5783393  
; GENERAL INFORMATION:  
; APPLICANT: Kelloff, Jill A.  
; APPLICANT: Bestwick, Richard K.  
; TITLE OF INVENTION: PLANT TISSUE / STAGE SPECIFIC PROMOTERS FOR  
; TITLE OF INVENTION: REGULATED EXPRESSION OF TRANSGENES IN PLANTS  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Avenue, Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/592,936B  
; FILING DATE: 29-JAN-1996  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Evans, Susan T.  
; REGISTRATION NUMBER: 38,443  
; REFERENCE/DOCKET NUMBER: 4257-0012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 324-0880  
; TELEFAX: (650) 324-0960  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2917 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear







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	DEFINITION	Sequence 32 from Patent M09743427.				
	ACCESSION	A67827				
	VERSION	A67827.1	GI:4756649			
	KEYWORDS					
SOURCE	ORGANISM	' thale cress. <i>Arabidopsis thaliana</i> Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; endicotsyledons; core endicots; Rosidae; eurosids II; Brassicales; Brassicaceae;				
REFERENCE	AUTHORS	Arabiopsis. 1 (bases 1 to 2089) De,V.S., Schmidt,E.D., Van,H.G. and Hecht,V.F. PRODUCTION OF APOMICETIC SEED Patent: WO 9743427-A-20-NOV-1997;				
JOURNAL	TITLE	CIBA GEIGY AG (CH)				
FEATURES	Source	Location/Qualifiers 1..2089 /organism="Arabidopsis thaliana" /db_xref="taxon:3702" /clone="SERK GENE CDNA" 195..2072 /note="unnamed protein product" /codon_start=1 /protein_id="CAB42254.1" /db_xref="gi:4756650" /translation="MESSYVFILSLILLPNHSLMASNLDEGDLHTLRVLVDNPN NTLOSMDPLVNPCPTMCTHMVCNNNSNYIRDLGAELSGHLVEPLGYLKNLOYLEIS NITNGIPSPNIGJLTNTFVIDIYNPSGPPELSGLPRLRLLNNSELGTSPMS LNRTTTLQVLDLSNNRLSCGYPDNGSSLETPIEFANNLDCGFVTSHPCGSEPPSR EPDETPPPVPSTPGSYGITGAIAGGVAGAALPPAADAIAFAAMRRSPIDIFEDVA EEDEVRIHQDKRELSRELQVASDFGNKNMLRGFGKYKGKLADGTVAKRKKE ESPTGGELQOTETEVMASMAVRMLRLRGFCMTPTERLVAVPYMANGSVASCLEERP EORCPLOMPTEPKRIAISARLSYLHHOCDPKIHRDYKANILLDEFEVVVDGFI AKLMDDYDTHTTTTGTCITBGCTIGHAEYSYGTSKSSTKTFVGIMLLLTIGORAFLDA PLAADDMVLMIDWKGLKKLKKEKLEMIVDPOLQTVERRELFQVVALYTLCQGSPMER PKSEEVRMLEGDGLARKWDEMQRVELIREBTDLPNPNSDWIIDSTLINHAVELSCP R"				
BASE COUNT	569 a	419 c	502 g	599 t		
ORIGIN						
Query Match	100.0%;	Score 2089;	DB 5;	Length 2089;		
Best Local Similarity	100.0%;	Pred. No. 0;				
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LOCUS DCU93048 1755 bp mRNA PLN 28-JUN-1997  
DEFINITION Dausus carota somatic embryogenesis receptor-like kinase mRNA,  
complete cds.  
ACCESSION U93048  
VERSION U93048.1 GI:2224910  
KEYWORDS  
SOURCE .  
ORGANISM carrot.  
Dausus carota  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core  
eudicots; Asteridae; euasterids II; Apiales; Apiales; Daucus.  
REFERENCE  
AUTHORS 1 (Bases 1 to 1755)  
Schmidt,E.D., Guzzo,F., Toonen,M.A. and de Vries,S.C.  
TITLE A leucine-rich repeat containing receptor-like kinase marks somatic  
Plant cells competent to form embryos  
JOURNAL Development 124 (10), 2049-2062 (1997)  
MEDLINE 97313247  
JOURNAL 2 (Bases 1 to 1755)  
Schmidt,E.D., Guzzo,F., Toonen,M.A.J. and de Vries,S.C.  
TITLE Direct Submission  
JOURNAL Submitted (12-MAR-1997) Molecular Biology, Agricultural University  
of Wageningen, Dreyenlaan 3, Wageningen 6703 HA, The Netherlands  
FEATURES  
source location/Qualifiers  
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34..1695

/note="SERK"  
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/product="somatic embryogenesis receptor-like kinase"  
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Query Match 44.78; Score 934.8; DB 8; Length 1755;  
Best Local Similarity 74.58; Pred. No. 3e-251;  
Matches 1192; Conservative 0; Mismatches 402; Indels 6; Gaps 1;  
Qy 486 ttgagacttlaacgaaacataactcgcgacttcctagtaattcttgaagaatcgaca 545  
Db 115 TTGAGGCTTTACAGCAATACATTAAGTGAGCAATTCCTAGTATCTTGGAAATCTGACA 174  
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Db	1549	GGTATGTGCTTGCAGAAAGTGGAGACGATGGCAAAAAGTGAAGCTCATCATCAAC	1608
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Db	1609	GTAACAAATTAGCTCCACATCCATCCATCTGTGATGATGATCTGTACCTCAGACGATTA	1668
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Db	1609	GCTTTGATATATCTGCTCCAAATATTAACGACTATATAA	1708
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DEFINITION	Sequence 2 from Patent WO9743427.	PAT	05-MAY-1999
ACCESSION	A67797		
VERSION	A67797.1	GI:4756623	
KEYWORDS			
SOURCE	carrot.		
ORGANISM	Daucus carota		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophytes; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asterales; euasterids II; Apiales; Apicaceae; Daucus.		
AUTHORS	De V.S., Schmidt E.D., Van H.G. and Hecht V.F.		

FEATURES	source	Location/Qualifiers
TITLE	PRODUCTION OF AROMATIC SEED	
JOURNAL	Ciba Geigy AG (CH)	
PATENT	WO 9743427-A 20-NOV-1997;	
source	1. 1815	
CDS	/organism="Daucus carota" /db_xref="taxon:4039" 94.1755 /codon_start=1 /note="unnamed protein product" /protein_id="CAB42241.1" /db_xref="GI:4756624" /translation="MNRNSINILNLMVOFTDAVLDKYGLMTLEYSNNISGELPSPDLG NLTVLSVLDLYMNFSGSPIDPTDGLKILRLFLRNLNNSLSGLPIMSLNTITLLOVLD SNNLSRPVDPNDSFSLFPISPANNINLIGCPYMGRCPSPPSPSPPISTQSP PGQNGPTGALAGVAGAGALLFPAAPAAFMWRNRKRREHFDPAEDEEVLGQLE RFSRELQVATDFTSTILGRGFEKVKYGRLAOSLYAVRLKEERTPGGELFOFTEV EMIAVAHRLNLRRLRGCPMTPTERILVYPMANOSVASCRLEROSPSPDLPWPKRI ALSGARGSYLHDDCPKIIHRVDKANIIILDEEFEEVYDGFGLARLMDYKLDHVTYA VRGLGTIAPELVLSTGSKSEKTDVEYGLMELTEIGORAFDLARLNDVDMLDMV KSLIKERKLEMLNDPLENNVTIDREYVOLLIOVALICDGSPPMERPKSEVYRLLEGDG LAEWDEMRQKVEYVHODVELAPRHTSMILDSIDNLHAFELSGR"	
BASE COUNT	531 a 354 c 415 g 515 t	
ORIGIN		
Query Match	44.7%: Score 934.8; DB 5; Length 1815;	
Best Local Similarity	74.5%: Pred. No. 3e-251;	
Matches 1192; Conservative	0; Mismatches 402; Indels 6; Gaps 1;	
486	ttgagactttaagaataacataactcgcgcgaattccagtaacttggaatctgaca	545
175	ttgagagctttacagaaataacataagtgagaccatttctagatctgggaactcgaca	234
546	aacttagtgagtttgatcttacttaaacgcttcccggtccattccggaatcaatg	605
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606	ggaagacttcaaacctgagatcttcctcgcgcgttcaacaaacagctcactcagtgatcaat	665
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666	ccatagtacatgacacaatatctactacccttcaagtgttagatctatacaataacagatc	725
355	ccaaatgctacacgacaaataatttcaactcttcaagctcggaattatttcaaacaaatcgcta	414
726	tctgttctagctcccgacaatgctcccttctacacttccaaacccatagtttggta	785
415	tcagagacacagatcccgatgataatggctcaatttctgtttacacatcagattttgccaat	474
786	aacttagacctatgtgagctggttaacaagtaaccgaatgctcctgagatctccccgtttct	845
475	aatttgaaatttatgtggaccccgtaactgggaagccctgcctcgatgctcccccaatttgcg	534
846	ccctcacacaccttatttcaacctcccccagtttccaaacccgagtgagtgatgataact	905
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906	ggaagcaataactgttgagagttgtgtcgaagtgctgcttggcccttggctgtcctcgaca	965
595	ggagctaatgtcggggagtagtacctgctggtgcttttactgatttgcgtcacctcgatg	654
966	gaccttgcttggttgagcgaagaagccacagatgattttcttcgattgctccgtcgcaa	1025
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1026	gaagatccagaagttcatctgtggaacagctcaagaggtttcttcttgcggaagctacaatg	1085
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1086	gcagatgtagtggttcaagtaacaagaacatttgggcgaagtggttggtaggaagttcac	1145
775	gcacagagctactttttagt-----acacattacttggaacaggttggtttggaaggtgtagt	828

OY	1146	aaggaacgcttggcagacgcggaactcttgttcgtcctaagaagactcyaaagaaagcgcaact	1205
Db	829	AAGGACGCCCTTGCTGTATGGCTCACTTGTGAAGCAGTTTAAAGAGCCCTTAAGAAGAACGAACA	888
OY	1206	cgaagtggagagccccaagttccaacaagaagtagagataatgatcatgacagttcacatcga	1265
Db	889	CCAGGTGGTAGCTGCAGTTTCACCAAGAGAGTGGAATATTATAGCATGGCTGTGCATCGA	948
OY	1266	aaccttgtagatcacgaagttcttcgtatcacaccgacccagagatalgcttgtytatcct	1335
Db	949	AATCTTGCAGTCAACTGGTCTTCTGCATGACACCMAAGACGGGCTTCTGTATATCCA	1008
OY	1326	tacattgccaatggaagtgtgtcttcgtgtgtcctcaagagagaagccacgltcaaacactcg	1385
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OY	1386	cttattggccaacgcggaagagaatccgcgtctaggctcagctcgaagtttcltctaacta	1445
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OY	1506	gacgaagaattcgaagcggtgtgtcttgtagattccggtgtggcaaacctatgyactataaa	1555
Db	1189	GACCAAAATTTTAAAGCTGTGTGAAGTGATTTTGGGTTAAGTAGGCTCATGATGATTAACAG	1248
OY	1566	gacactacgtgacaacgaagcagtcscgtgacacatcgcacatccgcaccaagaatatic	1625
Db	1249	GATACCCATTTTAAACATGCTGTAAAGGGTACTTGGCTAAATAGCTCCGAGTACTCTC	1308
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Db	1309	TCGACTCGAAAAGTCATCAGAGAAAGACCAGTGTCTTGGTTAAGGATTAATGCTCTTAGAG	1368
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Db	1429	TGTGTGATTGGGTTAAAGCCTTTTGAAGAAGAAAAATTGGAAATGCTGGTCAATCCT	1488
OY	1806	gattcttcaacaactacgcgagagagagaactcygaaacagtatcaaatgtyggcgttgcta	1865
Db	1489	GACCTGGAGAAACATTATACATTGTACACAGAAAGTGVGACACTTATCAAGTAGCATTAATC	1548
OY	1866	tgcgcgaagaagatcacaacaaatggagaagaaccaaaagatggtcgaagtgttaagatgtgaa	1925
Db	1549	TGTATCCACAGGGTTGGCCAAATGGAGCGGCTTAAGATGTCAAGAGTAGTCCGAATGCTTGAA	1608
OY	1926	ggagatgagcttcggaagaatctgagacgaatgccaanaagttggaatttgaaggaagag	1985
Db	1609	GGTGATGGCTTTCGACAAAAGTGGGACAGTGGCAAAAAGTAGAAGTCATCATCAAAAC	1668
OY	1986	atgagattgagtcctcaatccctaactctgattgtagtcttgaattacttaacaattgcac	2045
Db	1669	GTAATAATTACTCTCACATCCMACATCTTGATGATGATCTCTGACATCGACAGATAACTTGAT	1728
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Db	1729	GCTTTTCAATTATCTGSTCCAAAGATTAACAGCATATATAA	1768
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LOCUS	ACOL12654		PLN
DEFINITION	Arabidopsis thaliana chromosome 1 BAC F14023 sequence, complete		10-DEC-1999
ACCESSION	ACOL12654.2	GI:6554462	
VERSION			

KEYWORDS	HTG.
SOURCE	thale cress.
ORGANISM	Arabidopsis thaliana
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE	1 (bases 1 to 98471)
AUTHORS	Li, S.-X., Lee, J.-M., Sakano, H., Yu, G., Jha, V. A., Lenz, C., Toriumi, M., Chin, C., Chou, J., Choi, E., Gonzalez, A., Hong, B., Koo, T., Li, J., Liu, A., Phan, P., Vaysberg, M., Altafi, H., Brooks, S., Buehler, E., Chao, Q., Conn, L., Conway, A. B., Hansen, N., Johnson-Hopson, C., Khan, S., Kim, C., Lam, B., Nguyen, M., Palm, C., Shih, P., Tamunga, G., Davis, R. W., Ecker, J. R., Federspiel, N. A. and Theologis, A.
TITLE	Arabidopsis thaliana chromosome 1 BAC F14023 sequence
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 98471)
AUTHORS	Theologis, A.
TITLE	Direct Submission
JOURNAL	Submitted (02-NOV-1999) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
	3 (bases 1 to 98471)
AUTHORS	Theologis, A.
TITLE	Direct Submission
JOURNAL	Submitted (10-DEC-1999) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
COMMENT	On Dec 10, 1999 this sequence version replaced gl:6175131.
FEATURES	Location/Qualifiers
SOURCE	1. 98471
	/organism="Arabidopsis thaliana"
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Query Match	40.9%; Score 854.6; DB 8; Length 98471;
Best Local Similarity	84.6%; Pred. No. 1,8e-228;
Matches 1068; Conservative	0; Mismatches 4; Indels 191; Gaps 2.
QY 1018	ctgcggaagaagatccagaagtcacatcctcgtgagcagctcaagaagttctcttcgcgagc 1077
Db 79858	CAGCCGAAGAAGATCCAGAAGTTCAATCTGGAGCAGCTCAAGAGGTTTCTTGGGGAGC 79917
QY 1078	tacaagtcgagagtgatgggttagtaacaagaacatttggcagagtggtgtttgga 1137
Db 79918	TACAAAGGCGAGATGATGGGTAGTAAACAAACATTTTGGGAGAGGTGGGTTGGGA 79977
QY 1138	aagctcaaggagagccttggcagaagagacctgttgctgcttaagaagactaagaag 1197
Db 79978	AAGCTTCAAGGGAGCCTTGGCGAGCGAGACCTTGTGCTGTCAAGAGCTGAAGAGAG 80037
QY 1198	agcgaactcaggttggagagctccagtttccaacagaagtagagatgataagatgacg 1257
Db 80038	AGCGAATCCAGGTGAGAGCTCCAGTTTCAACAGAGAGTAGAATAGATGGCAG 80097
QY 1258	ttcatgaaacctgtttgagattacagagttcttgatagacaacgacccagagatgtctg 1317
Db 80098	TTTCATCAAAACCTGTTGAATATACGAGGTTCTGTATACACCGACCGAGAGATGCTGG 80157
QY 1318	tgatctcttcaatgagcgaatgaaatgtttgcttctgtgtcag----- 1361
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QY 1361	-----agagagcgaacgltacaacactcgcgttatt 1392

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 Db 80338 GCCCAACGGGGAAGAAATCCGGCTAGGCTCAGCTCGAGGTTGCTTACCTACATGATC 80397  
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 Db 81118 AAA 81120

RESULT 5  
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 LOCUS A67815  
 DEFINITION Sequence 20 from Patent WO9743427.  
 ACCESSION A67815  
 VERSION A67815.1 GI:4756638  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 thale cress.  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core  
 eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;  
 Arabidopsis.  
 REFERENCE 1 (bases 1 to 4081)

AUTHORS De V.S., Schmidt E.D., Van H.G. and Hecht V.F.  
 TITLE PRODUCTION OF APOMITIC SEED  
 JOURNAL Patent: WO 9743427-A 20-NOV-1997;  
 CIBA GEIGY AG (CH)  
 FEATURES  
 Location/Qualifiers  
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 /clone="ARABIDOPSIS SERK GENE"  
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 exon 2014..2085  
 exon 2203..2346  
 exon 2450..2521  
 exon 2617..2688  
 exon 2772..2884  
 exon 3015..3146  
 exon 3305..3646  
 exon 3760..4081  
 BASE COUNT 1120 a 770 c 785 g 1406 t  
 ORIGIN

Query Match 25.9%; Score 540.8; DB 5; Length 4081;  
 Best Local Similarity 85.3%; Pred. No. 1.2e-140;  
 Matches 665; Conservative 0; Mismatches 2; Indels 113; Gaps 1;

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 QY 1078 tacaagtgcgagatgagtggtttagtaacaagaacatttggcagagtggtttgga 1137  
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 QY 1318 tgratccttaactggccaatggaagtgtgcttgcgtcag----- 1361  
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 QY 1361 ----- 1361  
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Db 3962 AGACACTGACGTGCAACAGCAGTCCGTGGCACCACATGCTCACATGCTCCAGATAATCT 4021  
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LOCUS Arabidopsis thaliana chromosome 1 BAC F23M19 sequence, complete  
DEFINITION  
ACCESSION AC007454 GI:5091613  
VERSION AC007454.3  
KEYWORDS Htg.  
SOURCE thale cress.  
ORGANISM Arabidopsis thaliana  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core  
eudicots; Rosidae; eustosids II; Brassicales; Brassicaceae;  
Arabidopsis.  
REFERENCE 1 (bases 1 to 88401)  
AUTHORS Vysotskaya,Y.S., Schwartz,J.R., Yu,G., Toriumi,M., Lenz,C., Liu,S.,  
Lee,J., Liu,A., Li,J., Kremetskaya,L., Luros,J., Gonzalez,A.,  
Altaf,H., Araujo,R., Chao,Q., Conn,L., Conway,A.B., Dunn,P.,  
Hansen,N., Huizar,L., Kim,C., Palm,C., Rowley,D., Shin,P.,  
Walker,M., Davis,R.W., Ecker,J.R., Federspiel,N.A. and Theologis,A.  
Arabidopsis thaliana chromosome 1 BAC F23M19 sequence  
Unpublished (1999)  
2 (bases 1 to 88401)  
AUTHORS Theologis,A.  
JOURNAL Direct Submission  
Submitted (01-MAY-1999) Plant Gene Expression Center, 800 Buchanan  
Street, Albany, CA 94710, USA  
3 (bases 1 to 88401)  
AUTHORS Theologis,A.  
JOURNAL Direct Submission  
Submitted (04-JUN-1999) Plant Gene Expression Center, 800 Buchanan  
Street, Albany, CA 94710, USA  
4 (bases 1 to 88401)  
AUTHORS Theologis.  
JOURNAL Direct Submission  
Submitted (17-JUN-1999) Plant Gene Expression Center, 800 Buchanan  
St., Albany, CA 94710, USA  
COMMENT On Jun 17, 1999 this sequence version replaced gi:4996902.  
The sequence of BAC F23M19 from Arabidopsis thaliana chromosome 1.  
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EVANTIVKANLHMSLSKDSITHLKEVNLSEEVQNLISKMDLRLIAAKRRQHD  
PVTLYVQRDLVHLEHALDRFQDYQKIOEENPSTAQGVGTALIRTELKQOK  
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HAKKEKELATLIDLVVHLHIVYQVARTTCYGIKRSYKPSIRSPNKTIOSSGSHNP  
SMGLPLITEDQEMLRDVSRRKTPGISKSQSEFTYAKAKRLCKHRLKSSSHSPWMG  
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24842..24955,25045..25117,25210..25348,25453..25865,  
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11-MAR-1999  
Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5 (ESSA project).  
AL035678.1 GI:4490291  
thale cress.  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 96475)  
Beyan, M., Rose, M., Hempel, S., Ertlan, K.-D., Hoheisel, J., Mewes, H.W., Mannhaupt, G., Mayer, K.F.X. and Schueller, C.  
Unpublished  
2 (bases 1 to 96475)  
EU Arabidopsis sequencing, project.  
Direct Submission  
Submitted (11-MAR-1999) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: schueller@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de, Project Coordinator: Mike Beyan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UD Norwich, UK, E-mail: michael.beyan@bsrc.ac.uk  
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosome 4 can be viewed at: <http://websites.mips.biochem.mpg.de/proj/thal/>.  
Location/Qualifiers  
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RESULT 8  
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LOCUS Arabidopsis thaliana chromosome II section 77 of 255 of the  
DEFINITION complete sequence.  
AC006436 AE002093  
AC006436.4 GI:6598565  
VERSION HTG.  
KEYWORDS thale cress.  
SOURCE Arabidopsis thaliana  
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core  
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;  
Arabidopsis.

REFERENCE 1 (bases 1 to 65899)  
AUTHORS Lin, X., Kaul, S., Rounsley, S.D., Shea, T.P., Benito, M.-I., Town, C.D.,  
Fuji, C.Y., Mason, T.M., Bowman, C.L., Barnstead, M.E.,  
Fel'dby, T.V., Buell, C.R., Ketchum, K.A., Lee, J.J., Ronning, C.M.,  
Koo, H., Moffat, K.S., Cronin, L.A., Shen, M., Vanden, S.E., Umayan, L.,  
Tallon, L.J., Gill, J.E., Adams, M.D., Carrera, A.J., Creasy, T.H.,  
Goodman, H.M., Somerville, C.R., Copenhaver, G.P., Preuss, D.,  
Nierman, W.C., White, O., Eisen, J.A., Salzberg, S.L., Fraser, C.M. and  
Venter, J.C.  
TITLE Sequence and analysis of chromosome 2 of the plant Arabidopsis  
thaliana  
MEDLINE Nature 402 (6763), 761-768 (1999)  
REFERENCE 2 (bases 1 to 65899)  
AUTHORS Lin, X.  
JOURNAL Direct Submission  
COMMENT Submitted (13-DEC-1999) The Institute for Genomic Research, 9712  
Medical Center Dr., Rockville, MD 20850, USA  
On Dec 17, 1999 this sequence version replaced gi:4726109.  
The sequence and annotation of chromosome 2 were merged from those  
of the individual clones on this chromosome after removing  
overlaps. For detailed information, please see the TIGR web site  
(http://www.tigr.org/tdb/at/at.html).

Genes were identified by a combination of three methods: Gene  
Prediction programs including GRail  
(ftp://artur.epm.ornl.gov/pub/xgrail), GeneFinder (Phil Green,  
University of Washington), Genscan (Chris Burge,  
http://genomic.stanford.edu/GENSCAN.html), and NetPlantGene  
(http://www.cbs.dtu.dk/services/NetGene2/), searches of the  
complete sequence against a peptide database and plant EST  
databases at TIGR, and manual curations based on those analyses.  
Annotated genes are named to indicate the level of evidence for  
their annotation. Genes with similarity to other proteins are named  
after the database hits. Genes without significant peptide  
similarity but with EST similarity are named as 'unknown' proteins.  
Genes without protein or EST similarity, that are predicted by two  
or more gene prediction programs over most of their length are  
annotated as 'hypothetical' proteins. Genes encoding tRNAs are  
predicted as tRNAscan-SE (Sean Eddy,  
http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were  
identified by RepeatMasker (Arian Smit,  
http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes are  
numbered from the top to the bottom of the chromosome.

We thank the CSHL/MashU/ABI consortium for sequencing BAC clones  
F0P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone  
F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards  
and Satoshi Tabata for helpful assistance. In addition, we would  
like to thank the TIGR Bioinformatics Department, especially Lixin  
zhou, Hanif Khelak, Michael E. Heaney, Lily Fu, Feng Jiang, Jeremy  
Peterson, Michael Holmes, and Delwood Richardson for software and

database support.

This work was supported by the National Science Foundation,  
Department of Energy and the US Department of Agriculture.

Address all correspondence to: at@tigr.org.

#### FEATURES

Location/Qualifiers

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/organism="Arabidopsis thaliana"

/cultivar="Columbia"

/db\_xref="taxon:3702"

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Db 54707 TGAATTTAACTATCAAGCCTATCCTCATGCTG 54738

RESULT	9
LOCUS	SBRLK1
DEFINITION	SBRLK1 2278 bp mRNA
ACCESSION	Sorghum bicolor mRNA for protein serine/threonine kinase RLK1.
VERSION	Y14600.1 GI:5596995
KEYWORDS	protein serine/threonine kinase; RLK1 gene.
SOURCE	Sorghum.
ORGANISM	Sorghum bicolor

REFERENCE	1 (bases 1 to 2278)
AUTHORS	Annen,F. and Stockhaus,J
TITLE	SbRLK1, a receptor-like protein kinase of Sorghum bicolor (L.) Moench that is expressed in mesophyll cells
JOURNAL	Planta 208 (3), 420-425 (1999)
MEDLINE	99312726
REFERENCE	2 (bases 1 to 2278)
AUTHORS	Stockhaus,J.
TITLE	Direct Submission
JOURNAL	Submitted (14-M0G-1997) J. Stockhaus, Institut fuer Entwicklungs- und Molekularbiologie der Pflanzen, Heinrich-Heine-Universitaet, Universitaetstrasse 1, 40225 Duesseldorf, FRG
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eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;  
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REFERENCE 1 (sites)  
AUTHORS Nakamura,Y.  
TITLE Structural Analysis of Arabidopsis thaliana Chromosome 5. VI  
JOURNAL Unpublished (1998)  
AUTHORS 2 (bases 1 to 86064)  
TITLE Nakamura,Y.  
JOURNAL Direct Submission  
SUBMITTED (06-MAY-1998) to the DDBJ/EMBL/GenBank databases.  
Yasukazu Nakamura, Kazusa DNA Research Institute, Laboratory of  
Gene Structure 2; 1532-3, Yana, Kisarazu, Chiba 292, Japan  
(E-mail:ynakam@kazusa.or.jp, Tel:++81-438-52-3935,  
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JOURNAL	
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REFERENCE	1 (bases 1 to 6695)				
AUTHORS	De,V.S., Schmidt,E.D., Van,H.G. and Hecht,V.F.				
TITLE	PRODUCTION OF APOMICRITIC SEED				
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				AUTHORS	Federspiel,N.A., Davis,R.W., Conway,A.B., Palm,C.J., Conway,A.R.,
					Kurtz,D.B., Buehler,E., Dewar,K., Feng,J., Kim,C., Li,Y.,
					Sun,H., Ojima,O., Osborne,B., Shen,Y.K., Toriumi,M., Vyotskala,V.,
					Yu,G., Theologis,A. and Ecker,J.
				TITLE	Direct Submission
				JOURNAL	Submitted (05-JUN-1997) Biochemistry, Stanford University/DNA
					Sequencing and Technology Center, 855 California Avenue, Palo Alto,
					CA 94304, USA
				REFERENCE	3 (bases 1 to 120787)
				AUTHORS	Federspiel,N.A., Davis,R.W., Conway,A.B., Palm,C.J., Conway,A.R.,
					Kurtz,D.B., Buehler,E., Dewar,K., Feng,J., Kim,C., Li,Y.,
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					Yu,G., Theologis,A. and Ecker,J.
				TITLE	Direct Submission
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					Sequencing and Technology Center, 855 California Avenue, Palo Alto,
					CA 94304, USA
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					Au,M., Araujo,R., Brendel,V., Buehler,E., Dewar,K., Feng,J.,
					Kim,C., Li,Y., Ojima,O., Osborne,B., I., Shin,P., Sun,H., Toriumi,M.,
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					Sequencing and Technology Center, 855 California Avenue, Palo Alto,
					CA 94304, USA
				REFERENCE	5 (bases 1 to 120787)
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					Au,M., Araujo,R., Brendel,V., Buehler,E., Dewar,K., Feng,J.,
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					Sequencing and Technology Center, 855 California Avenue, Palo Alto,
					CA 94304, USA
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					Au,M., Araujo,R., Brendel,V., Buehler,E., Dewar,K., Feng,J.,
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					Vyotskala,V., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.
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VERSION AC002292.1 GI:2252639  
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REFERENCE  
AUTHORS Federspiel,N.A., Palm,C.J., Conway,A.B., Kurtz,D.B., Conway,A.R.,  
Au,M., Araujo,R., Brendel,V., Buehler,E., Dewar,K., Feng,J.,  
Kim,C., Li,Y., Ojima,O., Osborne,B.I., Shin,P., Sun,H., Toriumi,M.,  
Vyotskala,V., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.  
TITLE  
Genomic sequence of Arabidopsis  
JOURNAL  
Unpublished (1997)

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GenCore version 4.5  
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## OM nucleic - nucleic search, using sw model

Run on: June 23, 2000, 22:46:24 ; Search time 274.21 Seconds  
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Searched: 230463 segs, 6492525 residues

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
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## SUMMARIES

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## ALIGNMENTS

RESULT 1  
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: Patent No. 5977434  
: GENERAL INFORMATION:  
: APPLICANT: Ronald, Pamela C.  
: APPLICANT: Wang, Guo-Liang  
: APPLICANT: Song, Wen-Yuang  
: APPLICANT: Szabo, Veronique  
: TITLE OF INVENTION: Procedures and Materials for Conferring  
: TITLE OF INVENTION: Disease Resistance in Plants  
: NUMBER OF SEQUENCES: 27  
: CORRESPONDENCE ADDRESSES:  
: ADDRESSEE: Townsend and Townsend and Crew LLP  
: STREET: Two Embarcadero Center, Eighth Floor  
: CITY: San Francisco  
: STATE: California  
: COUNTRY: USA  
: ZIP: 94111-3834  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patentin Release #1.0, Version #1.30  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/587,680A  
: FILING DATE: 17-JAN-1996  
: CLASSIFICATION: 800  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/373,375  
: FILING DATE: 17-JAN-1995  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/475,891  
: FILING DATE: 07-JUN-1995  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 60/004,645  
: FILING DATE: 29-SEP-1995  
: PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: US 08/567,375  
: FILING DATE: 04-DEC-1995  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Bastian, Kevin L.  
: REGISTRATION NUMBER: 34,774  
: REFERENCE/DOCKET NUMBER: 023070-058940US  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (415) 576-0200  
: TELEFAX: (415) 576-0300  
: INFORMATION FOR SEQ ID NO: 24:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 1554 base pairs



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Db 1714 AATGAGGTGAGATTGATCCGAGGCTTCAGACATATATAACCTTGTCCGAAATTCTTGCTCT 1773
QY 1290 tgratgaacacgcagcagagatgtctgtatccttacatgccaatggaagtgtct 1349
Db 1774 TGCATTGAGGCAACACAGAAAGATGATGATATGATATTTAGAAATTTAGCCCTCGAT 1833
QY 1350 tctgtctcagagagagacacgcctccacacccctcctgattggtccaaacgcggaaga 1409
Db 1834 TCTTATCTCTTCGGAAATATAACG---AAGCTTACCTTAAATTTGGAGACAGATTTCAAC 1890
QY 1410 atcgcgtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1469
Db 1891 ATTACCAATGCTGCTCGAGAGCTTTTATATCTTCAATCAAGACTCAGGTTTAGGATA 1950
QY 1470 attcaccgtgaagcgaagaacgaacacacccctccttagcgaagaattcgaaagcgtgt 1529
Db 1951 ATCCACAGAGATATGAAATAGTAACTTTTCTTGATATAAATATGACACCAAGATC 2010
QY 1530 ggaattcggggttggcaagcctatgacataaagacactcacg---tgacaacagca 1586
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QY 1647 aaaaacgcagcttctcgatacggatcatcgtctcagaactaatcacaagacaagaagct 1706
Db 2131 AATTCAGATGTTTTCAGTTTGGAGTCATTTGTTGAATTTGTTAGTGAAGAAAGGAAC 2190
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Db 2191 AGAGGATTTTACACTTGAACCGAAGAAACAAATCTTAAGCTATGATAGGATCGACTGG 2250
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QY 1872 caagagtcacacatggaagaagcagaagatgtctgaagtgtgaagatgtgtgaagaagt 1931
Db 2371 CAGGAACGTGACAGCATAGACCAACAGATGTGCTCCGTGTTGGATGCTTGAAAGTGA 2430
QY 1932 g 1932
Db 2431 G 2431

RESULT 3
US-07-717-331F-9
; Sequence 9, Application US/07717331F
; Patent No. 5484905
; GENERAL INFORMATION:
; APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua
; APPLICANT: Stein
; TITLE OF INVENTION: A Receptor Protein Kinase Gene
; TITLE OF INVENTION: Encoded At The Self-Incompatibility Locus
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
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; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/717, 331F
; FILING DATE: June 19th 1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-07-717-331F-9

Query Match 4.4%; Score 92.6; DB 1; Length 2571;
Best Local Similarity 49.6%; Pred. No. 7.5e-19;
Matches 323; Conservative 0; Mismatches 319; Indels 9; Gaps 3;

QY 1110 aacatttggcgagaggtgtgttgggaagctcacaaaggaagcgttgcgaagcgaact 1169
Db 1594 AACCAATCTCGAACAAGGTTGTTGTTGTTTATCAAGGGGAATATCTTGACGGGAAA 1653
QY 1170 ctgtgtgtcgaagaagcctgaagaagcgaactccaggtgagagctccagttcaca 1229
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QY 1230 acagaagaagatgataagatgacagttcatcgaaacctgttgagattacgaagtttc 1289
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QY 1290 tgratgaacacgcagcagagatgtctgtatccttacatgccaatggaagtgtct 1349
Db 1771 TGCATTGAGGAGATGAAGATGTTGATATATGATATGTTGGAATTTAAAGCCTTGAT 1830
QY 1350 tctgttccagagagagccacgcgttcacaacctcgcgttgaattggccaacgcggaaga 1409
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Db 1888 ATTACCAATGCTGTTGCTCGAGGCTTTTATATCTTCAATCAAGACTCAGCGTTAGGATA 1947
QY 1470 attcaccgtgacgtaaaagcgaacacatcctcttagaagcagaagatccgaagcgtgt 1529
Db 1948 ATCCACAGAGATTTGAAAGTAAAGTAACTTTTGGCTTGCAAAAAATATGATCCCAAGATC 2007
QY 1530 ggaattcggggttggcaagcctatgacataaagacactcacg---tgacaacagca 1586
Db 2008 TCGGATTTTGGGATGCGCCAGATATTTGAAGGACGAAAGCAAGCTTAACACATATGAAG 2067
QY 1587 gtccgtgacacatggttcacatcgtctccagaatatctcacaacgcgaaatcttcagag 1646
Db 2068 GTGCTCGGAACATAGCGGCTACATGTCGCCGAATATGCAAGCAATGTATTCGCGAA 2127
QY 1647 aaaaacgcagcttctcgatacggatcatcgtctcagaactaatcacaagacaagaagct 1706
Db 2128 AATTCAGATGTTTTCAGTTTGGAGTCTATGTTCTTGAATTTGTTAGTGAAGAAAGAAC 2187
QY 1707 ttgcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1757
Db 2188 AGAGATTTCTACACTTGAGACTACGAAACGATCTCTTAAGCTATGATAGG 2238

RESULT 4
US-07-717-331F-1
; Sequence 1, Application US/07717331F
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; Patent No. 5484905
; GENERAL INFORMATION:
; APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua
; APPLICANT: Stein
; TITLE OF INVENTION: A Receptor Protein Kinase Gene
; TITLE OF INVENTION: Encoded At The Self-Incompatibility Locus
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/717,331F
; FILING DATE: June 19th 1991
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2833 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-07-717-331F-1
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Query Match 4.48; Score 92.6; DB 1; Length 2833;

Best Local Similarity 49.6%; Pred. No. 8e-19;

Matches 323; Conservative 0; Mismatches 319; Indels 9; Gaps 3;

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QY 1110 aacatttggcagagcgggttgggaagtcatacaggagccttggcagcaggaact 1169
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QY 1170 ctgtgtctgaagagagcgaaggaagcgaactccaggctggaagctccagttcaa 1229
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DB 1654 GAATTTGCAGTAAAGGCTATCAAAAGACGTCAAGGAGGAGCTGATG--AGTTTATG 1710
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QY 1230 acagaagtagagatgataagtagtcagttcaacgaacctgtgagattcagaggttc 1289
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DB 1711 AATGAGGTGACACTAATTTGCGAGGCTTACGATATATAAAGCTTGTTCAAGTCTTGCGCTGT 1770
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QY 1290 tgtatgacacgcagcagcagagattgtgtatccttaccatgccaatggaagtgct 1349
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DB 1771 TGCATTGAAGGAGATGAGTAAGTGTGATATATGAGTATTGGAAAAATTTAAAGCTTTAT 1830
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QY 1350 tctgtctcagagagagccaccgctcacacacctccgcttgaattggccaacgcggaagaga 1409
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QY 1410 atcgcgtagagctcagctcagaggttcttactacatgatacgtcagtcagcagaagatc 1469
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DB 1888 ATTACCAATGGTGTGCTCGAGGCGCTTTTAAATCTTCAAGACTCAGGGTTTATGAGATA 1947
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1470 attaccgtgaagtaagaagcgaacacactcctctagcaggaagattcgaagcggtgtt 1529
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1948 ATCCACAGAGATTTGAAAGTAAAGTAACTTTGCTTGACAAAAAATATGATCCCAAGATC 2007
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1530 ggaagtttcgggttgccaagcttatagactataaagacactcaag--tgacaacagca 1586
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DB 2008 TCGGATTTTGGATGGCCAGACATATTTGAAAGSGAGCAAAAGGAGCTTAACAAATGAG 2067
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DB 2068 GTGTCGGAACATACGGCTTACATGTCGCCGGAATACGAATGTATGGATTTCTTGGA 2127
QY 1647 aaaccgcagctttcgatagacatcgtcttcttaagaactaacatcagacagaagact 1706
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DB 2128 AATATCATATTTTTCAGTTTGGAGTCATATGTTCTTGAAATTTGTAGTGAAGAAGAAC 2187
QY 1707 ttcgattcgtcgcgtcagtagcagcagcagcagcagcagcagcagcagcagcagcag 1757
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DB 2188 AGAGGATTTTCAACCTTGACATCAAGAAACGATCTCTTAAGCTATGTATGG 2238
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RESULT 5

US-07-717-331F-4

; Sequence 4, Application US/07717331F

; Patent No. 5484905

; GENERAL INFORMATION:

; APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua

; APPLICANT: Stein

; TITLE OF INVENTION: A Receptor Protein Kinase Gene

; TITLE OF INVENTION: Encoded At The Self-Incompatibility Locus

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Yahwak & Associates

; STREET: 25 Skytop Drive

; CITY: Trumbull

; STATE: Connecticut

; COUNTRY: USA

; ZIP: 06611

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy Disk

; COMPUTER: Macintosh

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: Microsoft Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/717,331F

; FILING DATE: June 19th 1991

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: George M. Yahwak

; REGISTRATION NUMBER: 26,824

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (203)268-1951

; TELEFAX: (203)268-1951

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2749 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

US-07-717-331F-4

Query Match 4.48; Score 92; DB 1; Length 2749;

Best Local Similarity 50.7%; Pred. No. 1.2e-18;

Matches 302; Conservative 0; Mismatches 285; Indels 9; Gaps 3;

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QY 1170 ctgtgtctgaagagagcgaaggaagcgaactccaggctggaagctccagttcaa 1229
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DB 1672 GAATTTGCAGTAAAGGCTATCAAAAGACGTCAAGGAGGAGCTGATG--AGTTTATG 1728
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QY 1230 acagaagtagagatgataagtagtcagttcaacgaacctgtgagattcagaggttc 1289
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Db	617	TATCCAAAGAAAGGACGTGACTCTGATTCAAACCCATCTTAGACACAGTAGTGAAGAAAGAAC	676
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Qy	1660	tcggatacgaatcacyctctctagaact	1687
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## RESULT 9

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US-08-567-375-3
: Sequence 3-5, Application US/08567375
: Patent No. 5952485
:
: GENERAL INFORMATION:
:   APPLICANT: Ronald, Pamela C.
:   APPLICANT: Wang, Guo-Liang
:   APPLICANT: Song, Wen-Yuang
:   APPLICANT: Szabo, Veronique
:   TITLE OF INVENTION: Procedures and Materials for Confering
:   TITLE OF INVENTION: Disease Resistance in Plants
:   NUMBER OF SEQUENCES: 16
:   CORRESPONDENCE ADDRESS:
:   ADDRESSEE: Townsend and Townsend and Crew LLP
:   STREET: Two Embarcadero Center, Eighth Floor
:   CITY: San Francisco
:   STATE: California
:   COUNTRY: USA
:   ZIP: 94111-3834
:
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: PatentIn Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/08/567,375
:   FILING DATE: 04-DEC-1995
:   CLASSIFICATION: 800
:
: PRIOR APPLICATION DATA:
:   APPLICATION NUMBER: US 60/004,645
:   FILING DATE: 29-SEP-1995
:
: PRIOR APPLICATION DATA:
:   APPLICATION NUMBER: US 08/475,891
:   FILING DATE: 07-JUN-1995
:
: PRIOR APPLICATION DATA:
:   APPLICATION NUMBER: US 08/373,375
:   FILING DATE: 17-JAN-1995
:
: ATTORNEY/AGENT INFORMATION:
:   NAME: Bastian, Kevin L.
:   REGISTRATION NUMBER: 34,774
:   REFERENCE/DOCKET NUMBER: 023070-058930
:
: TELECOMMUNICATION INFORMATION:
:   TELEPHONE: (415) 576-0200
:   TELEFAX: (415) 576-0300
:
: INFORMATION FOR SEQ ID NO: 3:
:   SEQUENCE CHARACTERISTICS:
:     LENGTH: 3921 base pairs
:     TYPE: nucleic acid
:     STRANDEDNESS: single
:     TOPOLOGY: linear
:
:   MOLECULE TYPE: DNA (genomic)
:
:   FEATURE:
:     NAME/KEY: CDS
:     LOCATION: join(1..2676, 3520..3918)
:     OTHER INFORMATION: /product="Xa-21"
:
US-08-567-375-3

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Db	1198	ATTGGCTACMACATCTCTATCTCTGCACMACMAAATTTTGAAGGGTCTCTCCATCATCTG	1257
Oy	603	cttggaagacttcaagcgcgagattcttcgcgcttaaacagaacgcttcactctgata	662
Db	1258	TTGGGACAGCTTAAATAAACCCTTAGGCATTCTACTGCGCTACGAAACACACTTGAACGGTTG	1317
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Db	1318	ATMCCGTTGGCCATAGGAATAATCTACTGAACTTAATATCTTACTGCTGGCACCAACANA	1377
Oy	723	ctctctggttcagttcctgcgaatgctc	751
Db	1378	TTCACTGGTTGGATACCATATACACTCTCT	1406

## RESULT 10

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US-08-587-680A-3
: Sequence 3, Application US/08587680A
: Patent No. 5977434
:
: GENERAL INFORMATION:
:
: APPLICANT: Ronald, Pamela C.
: APPLICANT: Wang, Guo-Liang
: APPLICANT: Song, Wen-Yuang
: APPLICANT: Szabo, Veronique
: TITLE OF INVENTION: Procedures and Materials for Confering
: TITLE OF INVENTION: Disease Resistance in Plants
: NUMBER OF SEQUENCES: 27
:
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/587,680A
: FILING DATE: 17-JAN-1996
: CLASSIFICATION: 800
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/373,375
: FILING DATE: 17-JAN-1995
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/475,891
: FILING DATE: 07-JUN-1995
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/004,645
: FILING DATE: 29-SEP-1995
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/567,375
: FILING DATE: 04-DEC-1995
:
: ATTORNEY/AGENT INFORMATION:
: NAME: Bastian, Kevin L.
: REGISTRATION NUMBER: 34,774
: REFERENCE/DOCKET NUMBER: 023070-058940US
:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
:
: INFORMATION FOR SEO ID NO.: 3:
:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3921 base pairs
: TYPE: nucleic acid
:
: STRANDEDNESS: single

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? REFERENCE/DOCKET NUMBER: 02370-058910US
? TELECOMMUNICATION INFORMATION:
?   TELEPHONE: (415) 576-0200
?   TELEFAX: (415) 576-0300
? INFORMATION FOR SEQ ID NO: 1:
?   SEQUENCE CHARACTERISTICS:
?     LENGTH: 6256 base pairs
?     TYPE: nucleic acid
?     STRANDEDNESS: single
?     TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
?   NAME/KEY: CDS
?     LOCATION: join(1648..4383, 5178..5513)
?   OTHER INFORMATION: /product= "PRR-F"
?   OTHER INFORMATION: /note= "xa21 Xanthomonas spp. disease
?     resistance gene PRR-F from rice (Oryza
?       sativa)"
? OS-08-475-891A-1

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Query Match	3.48;	Score 70.6;	DB 3;	Length 6256;
Best Local Similarity	53.9%;	Pred. No. 1.2e-11;		
Matches 145;	Conservative	0;	Mismatches 124;	Indels 0;
				Gaps 0

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QY	543	acaactttagtgagtttgatctcttaacttaaaagcttcocggtctattccggaatca	602
Db	2866	ATTGGCTTACAAACATCTCTCTCTGCAACAACAAATTTCAGAGGGTCATTCAATCATCG	2922
QY	603	ttagggaagcttccaagcggagattctccggttaaaacaaacagtcactcgtgca	662
Db	2926	TTGGGCGAGCTTAGAAACTTAGGCATTTCTAGTCGCTTACGAAACCACTTGAGCGGTTCG	2988
QY	663	attccctatgcatcgaaccaattactacccttcaagtgltgatctatcaataacaga	722
Db	2986	ATCCCAATGGCGCATAGGAATCTTACTGAACCTTAATATCTTACTGCTGGCACCAACAA	3045
QY	723	ctctctggttcagttcctgcaatgctc	751
Db	3046	TTTCAGTGTTGGATACCAATCAACACTCTC	3074

RESULT 13  
 US-08-567-375-1  
 Sequence 1, Application US/08567375  
 Patent No. 5952485  
 GENERAL INFORMATION:  
 APPLICANT: Ronald, Pamela C.  
 APPLICANT: Wang, Guo-Liang  
 APPLICANT: Song, Wen-Yuang  
 APPLICANT: Szabo, Veronique  
 TITLE OF INVENTION: Procedures and Materials for Confering  
 TITLE OF INVENTION: Disease Resistance in Plants  
 NUMBER OF SEQUENCES: 16  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/567,375  
 FILING DATE: 04-DEC-1995

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CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
FILING DATE: 29-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-058930
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6256 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: join(1648..4383, 5178..5513)
OTHER INFORMATION: /product="RRK-F"
OTHER INFORMATION: /note="Xa21 Xanthomonas spp. disease
resistance gene RRK-F from rice
(Oryza sativa)"
OTHER INFORMATION:

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Best Local Similarity	53.98;	Pred. No. 1.2e-11;		
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RESULT 14  
 US-08-587-680A-1  
 : Sequence 1, Application US/08587680A  
 : Patent No. 5977434  
 : GENERAL INFORMATION:  
 : APPLICANT: Ronald, Pamela C.  
 : APPLICANT: Wang, Guo-Liang  
 : APPLICANT: Song, Wen-Yuang  
 : APPLICANT: Szabo, Veronique  
 : TITLE OF INVENTION: Procedures and Materials for Confering  
 : TITLE OF INVENTION: Disease Resistance in Plants  
 : NUMBER OF SEQUENCES: 27  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/587,680A  
FILING DATE: 17-JAN-1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/373,375  
FILING DATE: 17-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/475,891  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/004,645  
FILING DATE: 29-SEP-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/567,375  
FILING DATE: 04-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 023070-058940US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6256 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1648..4383, 5178..5513)  
OTHER INFORMATION: /product= "RRK-F"  
OTHER INFORMATION: /note= "Xa21 Xanthomonas spp. disease  
OTHER INFORMATION: resistance gene RRK-F from rice (Oryza  
OTHER INFORMATION: sativa)"  
US-08-587-680A-1

Query Match 3.4%; Score 70.6; DB 4; Length 6256;  
Best Local Similarity 53.9%; Pred. No. 1.2e-11;  
Matches 145; Conservative 0; Mismatches 124; Indels 0; Gaps 0;  
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QY 543 acaactatgagagtttgatcttacttaaacagcttctccgctctacttcggaatca 602  
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QY 723 ctctctggttcagttctccagacaatggtc 751  
DB 3046 TTCAAGTGGTGGATACCATACACTCTC 3074

RESULT 15  
US-08-030-096-5/c  
Sequence 5, Application US/08030096  
Patent No. 5426041  
GENERAL INFORMATION:  
APPLICANT: Fabljanski, Steven F.  
APPLICANT: Arnison, Paul G.  
TITLE OF INVENTION: BINARY CRYPTOCYTOTXIC METHOD OF HYBRID  
TITLE OF INVENTION: SEED PRODUCTION  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington, D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/030,096  
FILING DATE: 22-MAR-1993  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/556,917  
FILING DATE: 20-JUL-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/CA91/00255  
FILING DATE: 22-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Bent, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 33229/164/PLHI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3641 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(854..1105, 1266..2375, 2463..2779)  
US-08-030-096-5

Query Match 3.3%; Score 68; DB 1; Length 3641;  
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Matches 235; Conservative 0; Mismatches 210; Indels 11; Gaps 3;  
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QY 1742 catgttacttgactgggtgaaaggatgtgtgaaggagaagctagagatgttagtga 1801
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Search completed: June 23, 2000, 22:47:16  
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## RESULT 2

V06571  
ID V06571 standard; cDNA: 1814 BP.  
AC V06571;  
DT 03-AUG-1998 (first entry)  
DE Dausus carota SERK gene.  
KW receptor kinase; apomixis; apomictic; seeds; production; embryos;  
OS Dausus carota.  
FH key  
FT CDS Location/Qualifiers  
FT 94..1755  
FT /tag= a  
FT /product= SERK protein

PN W09743427-A1.  
PD 20-NOV-1997.  
PE 13-MAY-1997; E02443.  
PR 14-MAY-1996; GB-010044.  
PA (NOVS ) NOVARTIS AG.  
PI De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ;  
DR WPI; 98-086529/08.  
PR P-PSDB; W47013.  
PS Production of apomictic seeds - useful in plant breeding  
PS Claim 21: Pages 47-51: 123pp; English.  
CC The sequence is that encoding SERK, a putative receptor kinase.  
CC It may be used as part of a method of producing apomictic seeds  
CC comprising: (a) transforming plant material with a nucleotide  
CC sequence encoding a protein which in active form in a cell or  
CC the membrane renders the cell embryogenic; (b) regenerating  
CC the transformed material into plants or carpel-containing  
CC plant parts; and (c) expressing the sequence in the vicinity  
CC of the embryo sac. The apomictic seeds and embryos thus produced  
CC can be developed into plant progeny. This is useful in plant  
CC breeding programs. Controllable and reproducible apomixis provides  
CC many advantages in plant improvement and cultivar development in  
CC the case that sexual plants are available as crosses with the  
CC apomictic plant. Apomixis provides for true-breeding, seed  
CC propagated hybrids and could shorten and simplify the breeding  
CC process so that selfing and progeny testing to produce and/or  
CC stabilise a desirable gene combination could be eliminated.  
CC Apomixis allows plant breeders to develop cultivars with  
CC specific stable traits for such characteristics as height,  
CC seed and forage quality and maturity.  
SQ Sequence 1814 BP; 530 A; 354 C; 415 G; 515 T;

Query Match 44.7%; Score 933.8; DB 1; Length 1814;  
Best Local Similarity 74.3%; Pred. No. 2.2e-230;  
Matches 1191; Conservative 0; Mismatches 402; Indels 6; Gaps 1;  
QY 486 ttggagcttcaagtaacataactgagccgagttctagtaacttggaaatcaca 545  
DB 175 TTGAGGCTTTACAGCAATACCAATAGTGACCAATTCCTAGTATCTGGGAATCTGACA 234  
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DB 355 CCAATGTCACTGACATAATATTACAACTTCAAGTCTCGATTATCAAAACAAATCGGCTA 414  
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DB 1189 GACGAAAGATTTGAGGCTGTGTGATGATTTTGAGTTAGCTTAGGCTCATGAGATTACAG 1248  
QY 1566 gacactcagctgacacacagcagctcgtgacacacacacacacacacacacacacac 1625  
DB 1249 GATACCCATGTACAACAGCTGATTAAGGGTACCTGGGCTACATAGCTCCGAGTACTC 1308  
QY 1626 tcaacggaaatcttcaagagaacacgacgcttctggatcaggaatcagcttctaga 1685  
DB 1309 TCGACTGGAAGTCAATCAGAGAGAACGATGCTTGTGTTGGATTTAGCTTTAAGAG 1368  
QY 1686 ctaatcaacagcaagaagcttgcctcgcctgcgtcagtagtaacagcagcagctcatg 1745  
DB 1369 CTCATTACGGACAGAGAGCTTTTGAATCTGTCCCTTGGGAACGATGATGATGATG 1428  
QY 1746 ttaacttgactgggtgaagagattgtgaagaagaagctagagatgtagttagatcca 1805  
DB 1429 TTGTTGATTTGGGTTAAAGAGCTTTTGAAGAGAAAGTTGAGAGATGCTGATCCT 1488  
QY 1806 gacttcaaaacaaactagagagagagaaacttgaaacagtgatatacaagtggcgctgta 1865  
DB 1489 GACCTGGAGAACAAATTTACATTTGACACAGAGTTGAGCAGCTTATTCAGATGACTT 1348  
QY 1866 tgcagcagaagatccacaactggaagaacccaagatgctgaagttgaagatgctgga 1925  
DB 1549 TGAACCAAGGTTTCCCAATAGAGGCGCTTAAGATGTCAGAGTAGTCCGAATGCTGAA 1608  
QY 1926 ggaagatggcttgcgagagaatggaagaatggaagaagaagttgagatttgaaggaag 1985  
DB 1609 GGTGATGGCTTGCAGAAAGTGGAGAGTGGCAAAAGTAGAAGATCATCATCAAGAC 1668  
QY 1986 attgattgagctccatccatcaactcattgattcttgaattcttaactcaaatcag 2045  
DB 1669 GTAGATTTAGCTCCACATCAGAGACTTCTGAATGAGATCCTAGAGCTGACAGATTA 1728  
QY 2046 gccgttgagatctcgtgtccaagtaaaaaa 2084  
DB 1729 GCTTTGAATTTATCTGCTGTCACAGATTAACAGCATATTA 1767

RESULT 3

ID	Accession	Standard	DNA	BP
V06585	V06585	standard	DNA	4081 BP
AC	V06585			
DT	03-AUG-1998	(first entry)		
DE	Arabidopsis thaliana SERK gene.			
DE	receptor kinase; apomixis; apomictic; seeds; production; embryos;			
KW	plant breeding; ds.			
OS	Arabidopsis thaliana.			
PH	Key	Location/Qualifiers		
FT	CDS	366..6620		
FT		/*tag= a		
FT		/note= "contains introns"		
FT	Intron	3731..3802		
FT		/*tag= b		
FT		/number= 1		
FT	Intron	3851..3979		
FT		/*tag= c		
FT		/number= 2		
FT	Intron	4124..4211		
FT		/*tag= d		
FT		/number= 3		
FT	Intron	4284..4357		
FT		/*tag= e		
FT		/number= 4		
FT	Intron	4430..4528		
FT		/*tag= f		
FT		/number= 5		
FT	Intron	4642..4757		
FT		/*tag= g		
FT		/number= 6		
FT	Intron	4890..4967		
FT		/*tag= h		
FT		/number= 7		
FT	Intron	5295..5803		
FT		/*tag= i		
FT		/number= 8		
FT	Intron	6197..6339		
FT		/*tag= j		
FT		/number= 9		
PN	W09743427-A1.			
PD	20-NOV-1997.			
PE	13-MAY-1997; E02443.			
PR	14-MAY-1996; GB-010044.			
PA	(NOVS ) NOVAPRIS AG.			
PI	De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ;			
DR	WPI: 98-086529/08.			
P-PSDB	W47017.			
PT	Production of apomictic seeds - useful in plant breeding			
PS	Claim 26; Pages 64-67; 123pp; English.			
CC	It may be used as part of a method of producing apomictic seeds			
CC	comprising: (a) transforming plant material with a nucleotide			
CC	sequence encoding a protein which in active form in a cell or			
CC	cell membrane renders the cell embryogenic; (b) regenerating			
CC	the transformed material into plants or carpel-containing			
CC	plant parts; and (c) expressing the sequence in the vicinity			
CC	of the embryo sac. The apomictic seeds and embryos thus produced			
CC	can be developed into plant progeny. This is useful in plant			
CC	breeding programs. Controllable and reproducible apomixis provides			
CC	many advantages in plant improvement and cultivar development in			
CC	the case that sexual plants are available as crosses with the			
CC	apomictic plant. Apomixis provides for true-breeding, seed			
CC	propagated hybrids and could shorten and simplify the breeding			
CC	process so that selfing and progeny testing to produce and/or			
CC	stabilise a desirable gene combination could be eliminated.			
CC	Apomixis allows plant breeders to develop cultivars with			
CC	specific stable traits for such characteristics as height,			
CC	seed and forage quality and maturity.			
Sequence	4081 BP; 1120 A; 770 C; 785 G; 1406 T;			

Query Match 25.9%; Score 540.8; DB 1; Length 4081;

Best Local Similarity 85.3%; Pred. NO. 1e-140;

Matches	665; Conservative	0; Mismatches	2; Indels	113; Gaps
OY 1018	ctcgcgagaagaatccagaagtcatcatctcggagacagctaagaagttcttcttcgaggagc			1077
Db 3302	CAGCGGAGAAAGATCCAGAAATCTTGGGACACCTTCMAAGAGTTTCTTTCGGGAGC			3361
OY 1078	tacaagtcggagtcgtatgtagtttaataacaagaacattcttggcagaggtcgggttcggga			1137
Db 3382	TACAAAGTCGGGATGATGGGTTTAGTAACAGAACATTTTGGGAGAGGTCGGTTGGGA			3421
OY 1138	aagtcctacaaggagcgttcggacaagcaactctgtctgcgtcaagaagacgaaaggaag			1197
Db 3422	AAGCTCTCAAGGGAGCCTTGGCAGACGGAACTCTGTTCGTCAAGAGACTGAAGAGAG			3481
OY 1198	agcgaaatccaagttgaaagagctccagtttcaacaagaaagtagaatatgaatgtagcag			1257
Db 3482	AGCGAACTCCAGGTCGAGGACCTCCAGCTTTCACACAGAAATGAAATGATGATGTGGCAG			3541
OY 1258	tctacgcgaacccgtttgaaattacgaggttctcgtatbacccgcagccagagattgcttg			1317
Db 3542	TTTCATCGAAACCTGTTGAGATTCGAGGTTTCTGTATGACACCCAGCAGAGATTGGCTT			3601
OY 1318	tgtatcctcatatcgtggccaatggaagtgtgtcgtcgtcgtcgaag-----			1361
Db 3602	TGTATCTTACATATGCGCAATGGAAGTGTGCTGTGCTCAGAGGTAACAACTAAACAA			3661
OY 1361	-----			1361
Db 3662	TTAAACATCTTGTGCTCTCTCTCAATTACTTGACGTGAAGTGTCTTTCATGTTTCTCT			3721
OY 1361	-----			1384
Db 3722	TTATGGGTCATATATGTTGGTTACTCATATGACACAGAGAGGCGACCGTCACAACTCC			3781
OY 1385	gcttgattcggccaagcgcggaagaatcgcgcgtagcctcagctcaggttgcgttaact			1444
Db 3782	GCTTGATTGGCCAAACGGGAGAGGAATTCGGCTAGCGTCACTCGAGGTTTGCTTTACT			3841
OY 1445	acatgatcaactcgcgtatccgaagatcatltaaccgtgtagttaaagcagcgaacatccctct			1504
Db 3842	ACATGATCAGCTGGGATCCGAAAGTCATTTACCGTAGACGTAAACGACGAAACATCCCTTT			3901
OY 1505	agacgaagaattcgaacgcgttcttgagatctcgggttcgggttcgcaagctatgagactaa			1564
Db 3902	AGACGAAGAATTCGAACCGGTTTGTGGAATTCCTGGGTTGGCAAAAGTAATGAGACTATA			3961
OY 1565	agacactcaactgtagcaacagcagtcgcgtgagcaacatcggtcaacatcgctccagaatact			1624
Db 3962	AGACACTCAGCTGTGCAACACACAGCACTCCGTGGCACATTCGGTACATCGCTCCAGAAATCT			4021
OY 1625	ctcaaccggaaaatcttcagagaagaacccaagtttcggatagagaatcattgctctaga			1684
Db 4022	CTCAACCGGAAATCTTCAGAGAAACCGACGCTTTCGGATACGGAAATCATCTTCTAGA			4081
RESULT 4				
VT ID	V06570			
AC	V06570; standard; DNA; 6695 BP.			
DT	03-AUG-1998 (first entry)			
DE	Daucus carota SERK gene.			
KW	receptor kinase; apomixis; apomictic; seeds; production; embryos;			
OS	Daucus carota.			
PM	Key			
FT	CDS	Location/Qualifiers		
FT		3696..6620		
FT		/*tag= a		
FT		/note= "contains introns"		
FT		3731..3802		
FT		/*tag= b		
FT		/number= 1		
FT		3851..3979		
FT		/*tag= c		
FT		intron		



Query Match	10.1%	Score 211.8	DB 1	Length 788
Best Local Similarity	63.0%	Pred. No. 2e-49		
Matches 327	Conservative 0	Mismatches 192	Indels 0	Gaps 0
Qy 270 gctaatttggaagrgatgagcttgcatactttagaggttacttgaagcttgaagcttgaacaaat	329			
Db 86 GCMAACTCCGAGAGGAGATGCTTTACGCTCTTCGCCGAGATTACAGATCCGACCAT	145			
Qy 330 gcttcgagagcttggatctcactagtagtaaccccttgacacatggttccatgtaacttgc	389			
Db 146 GTTTCACAGAGCTGGGATCCAACTCTGTTATTCCTTGACTGGTTCATGTCACTGT	205			
Qy 390 aacaacagagaacagtgataagagttgatttggggatgacagagttatctgccaatta	449			
Db 206 AACCAAGACMACCGGCTCTCGTGTGGATTTGGGGAAATTCAAACCTCTTGACATCTT	265			
Qy 450 gtccagagagcttgggtgtgtctcaagaatttgcagatttggagctttacagtaacacata	509			
Db 266 GCGCTGAGCTTGGGAGAGCTTGAACATTTCAGTATCTGAGCTCTACAAAACACATTC	325			
Qy 510 actggcccgatctccatagtaatcttggaaactgcgaacacttgaagtttggatcttac	569			
Db 326 CAAGGAACATATACCTCCGAACCTGGAATTCGAAGAATCATCATGAGCTTGATCTGAC	385			
Qy 570 ttaaacagcttccgggtctcattccgggaatatttgggaaagcttcaagcttgagatt	629			
Db 386 AACCAACATCTTACAGGGATGATGCTCCACTTCTTTGGGAAATTCAGTCTTGCTCTT	445			
Qy 630 ctccggcttaacaacacagctcactggtgataatctcattgcactgacccaattact	689			
Db 446 TTACGGCTTAATGACAACCGATTGACGGGGCCAATCCCTAGAGCACTCCTGCATCCCA	505			
Qy 690 acccttcaagtttagatctatccaataacagactctctgttcagcttcctgaatgac	749			
Db 506 AACCTTAAAGTTGTGATGCTCTCAAGCAATGATTTGTGTGGAACAATCCCAACAAACGA	565			
Qy 750 tccctcactcttcaaccacatcagtttggtaataac	788			
Db 566 CTTTTCCTACATTCCTTTACAGAACTTTGAGAACAC	604			
RESULT 6				
ID V06590				
AC V06590	standard; cDNA to mRNA; 1063 BP.			
DT 03-AUG-1998	(first entry)			
DE Arabidopsis thaliana SERK LRR homologous EST clone.				
KW receptor kinase; apomixis; apomictic; seeds; production; embryos;				
OS Arabidopsis thaliana.				
PM key	location/Qualifiers			
FT CDS	106..762			
FT FT	/tag= a			
FT FT	/note= "shows high homology to SERK"			
PN WO9743427-A1.				
PF 20-NOV-1997.				
PD 13-MAY-1997: E02443.				
PR 14-MAY-1996; GB-010044.				
PA (NOVS) NOVARTIS AG.				
PI De Vries SC, Hecht VFG, Schmidt EDL, Van Holst GJ;				
DR WPI: 98-086529/08.				
DR P-PSDB; W47022.				
PT Production of apomictic seeds - useful in plant breeding				
PS Claim 28; Pages 86-88; 123pp: English.				
CC The sequence is that of an EST clone showing high homology to				
CC SERK LRR (leucine-rich repeat) sequences.				
CC Sequence 1063 BP; 313 A; 242 C; 206 G; 302 T;				

QY	270	gctaatttggaagtgatgagcttctgatactcttgagggttactcttagttgataccaacaat	329
Db	184	GCMAAATCCGGAAGGAGATGCTTTACCGCTCTTCCCGGAGTTAAACAGATCCGACAT	243
QY	330	gtcttgagagcttgatgattcctacgctagtgaaatcccttgacatggtttcatgctctgc	389
Db	244	GTTCTCCAGAGCTGGGATCCAACTTTGTTAATCTTTGTTACTGGTTCCATGTCACTGT	303
QY	390	aacaacgaaagtgatcataagagttgatttggtggaaatgcagagttatctggtccatt	449
Db	304	AMCAAGAACAAACGGCTACCTGCTGGATTTGGGGAATTCAAACCTCTGAGACATCTT	363
QY	450	gttcagagcttggtggtcctcaagaatttgcaatcttgagctttgagcttcaagtaacaata	509
Db	364	GGCGCTGAGCTGGGAAGCTTGACATTATACGATATCTAGACCTCTTACAAAAACAATC	423
QY	510	actggtccgagatccctcagtaatctcttgaaatctgcgaaactgagatgagttgattac	569
Db	424	CAGGAAGACTATACCTTCGGAACCTTGGAATCTGGAAGAAATTCATACGCTTGATGTGAC	483
QY	570	ttaaacagctctccggtctcattctccggaatcatctgggaaagcttcaagctgagatt	629
Db	484	AMCAACAATCTTACAGGGGATTACTTCCACTTCTTGGGAAATTCGAATCTGCTCTT	543
QY	630	ctcggcttaacaacaacagctctcactggtggaattctctatgcatctgacccaattact	689
Db	544	TTACGGCTTAATGAAACACCGATTTGACGGGGCCAAATCCCTAGAGCACTCATGCCATCCCA	603
QY	690	acccttcagatgttgatctatcatcaataacagacctctggtctgagcttcctgacaatgac	749
Db	604	ACCCTTAAGTGTGTGATGCTCTCAAGCAATGATTGTGTGGGAACAATCCCAACAACGGA	663
QY	750	tctctcactctctcacaccatcactgatttgctaaataac	788
Db	664	CCTTTTGCCTACATTCCTTTTACAGAACTTGGAAACAAC	702
RESULT	7		
ID	V06587		
AC	V06587	standard; cDNA to mRNA; 981 BP.	
DT	03-AUG-1998	(first entry)	
DE	Arabidopsis thaliana SERK LRR homologous EST clone.		
KW	receptor kinase; apomixis; apomictic; seeds; production; embryos;		
OS	Arabidopsis thaliana.		
RFH	key	location/Qualifiers	
FT	CDS	104..760	
FT	FT	/*tag= a	
FT	PD	/note= "shows high homology to SERK"	
PD	WO9743427-A1.		
PR	20-NOV-1997.		
PR	13-MAY-1997.	E02443.	
PR	14-MAY-1996;	GB-010044.	
PA	(NOVS ) NOVARTIS AG.		
PI	De Vries SC, Hecht VEG, Schmidt EDL, Van Holst GJ;		
DR	WPI; 98-086529/08.		
DR	P-PSDB: W47019.		
PT	Production of apomictic seeds - useful in plant breeding		
CC	Claim 28; Pages 75-77; 123pp.	English.	
CC	The sequence is that of an EST clone showing high homology to		
CC	SERK LRR (leucine-rich repeat) sequences.		
SO	Sequence	981 BP; 286 A; 236 C; 180 G; 279 T;	

Query Match	10.1%	Score 211.8;	DB 1;	Length 1063;
Best Local Similarity	63.0%;	Pred. No. 2,3e-49;		
Matches 327; Conservative	0;	Mismatches 197;	Indels 0;	Gaps 0;
Sequence	1063 BP;	313 A;	242 C;	206 G;
				302 T;

	Query Match	10.1%	Score 210.2	DB 1	Length 981
	Best Local Similarity	62.8%	Pred: No. 6.2e-497		
	Matches 326	Conservative	0	Mismatches 193	Indels 0
					Gaps 0
QY	270	gctaatttgaagatgatgctttgcataactttgagggatctactctatgttgatccaacaat	329		
DB	182	GCAAATCTCGAAGGAGATCTCTTACAGCTCTTCCCGAGATTTCACGATCAACACCAT	241		

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QY 330 gtcttcagagctggagctctacgcgtagtgaaacctgacatggtcttcacgtcgtgc 389
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 242 gtccctccagagctggagctccacactctgttaacctctgacgttgccatgacactgt 301
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 390 aataacgagaacagctgcttaagatgcttggtggaatgcagagatctatcgtgccattta 449
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 AACCAAGACACCGCGCTACCTCGTGGATTTGGAAATTCCTGACATCTT 361
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 450 gtccagagctggtggtcaagaattgacagatcttggaatctgacatgaatgaacata 509
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 362 GCGCCGACGCTTGGAGAGTTTGACATTTACAGTATCTAGACCTGTACAAAACACATTC 421
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 510 actgcccagctctcgtatgaatctctggaatctgcacaactagtgagtttgatcttaac 569
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 422 CAAAGCAATCTACCTCCACACTTGGAAATCTGAAGAACTCATGAGCTTGATCTGTAC 481
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 570 ttaaacagctctccggtctctatctcgaatcattggaagaacttcaagctgagattt 629
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 482 AACCAACATCTTACAGAGATGTTCCACTTCTTGGGAAATTCAGTCTTGCTCTTT 541
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 630 ctccgcttaacacacacagctctcagctggttcaatctcattgcaatgaatattact 689
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 542 TTACGGCTTAATGACACCGATTTGACCGGTCCATCCCTAGAGACATCAGCGCAATCCCA 601
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 690 acccttcaagtgtagatctatcaataacagactctcgtgttcagttccctgcagaatgyc 749
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 602 AGCTTTAAAGTGTGTGACGTCTCAAGCAATGATTTGTGTGGAAATCCCAACAAACGGA 661
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 750 tccctcactcttcacacccatcagtttgcataaac 788
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 662 CCCTTGTGTCACATTCCTTTACAGAACTTTGAGAACAAAC 700
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 8
V06586 standard; cDNA to mRNA; 1106 BP.
ID V06586;
AC V06586;
DT 03-AUG-1998 (first entry)
DE Arabidopsis thaliana SERK LRR homologous EST clone.
KW receptor kinase; apomixis; apomictic; seeds; production; embryos;
KW plant breeding; leucine-rich repeat; ss.
OS Arabidopsis thaliana.
FH Key Location/Qualifiers
FT CDS 142..798
    /tag=a
    /note="shows high homology to SERK"
PN WO9743427-A1.
PD 20-NOV-1997.
PR 13-MAY-1997; E02443.
PR 14-MAY-1996; GB-010044.
PA (NOVS) NOVARTIS AG.
PI De Vries SC, Hecht VRG, Schmidt EPL, Van Holst GJ;
DR WPI: 98-086529/08.
DR P-PADB: W47018.
PT Production of apomictic seeds - useful in plant breeding
PS Claim 28; Pages 71-73; 123pp; English.
CC The sequence is that of an EST clone showing high homology to
CC SERK LRR (leucine-rich repeat) sequences.
SQ Sequence 1106 BP; 331 A; 258 C; 206 G; 311 T;

Query Match 9.1%; Score 191; DB 1; Length 1106;
Best Local Similarity 60.5%; Pred. No. 1.5e-43;
Matches 314; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

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QY 390 aacaacagagacagctgctcataaagattgatttggggaatgcagagttatctggtccattta 449
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 340 AACCAAGACACCGCGCTACCTCGTGGATTTGGAAATTCCTGACATCTT 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 450 gtccagagctggtggtcaagaattgacagatcttggaatctgacatgaatgaacata 509
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 400 GCGCTGAGCTTGGAGAGCTTGAACATTTTACAGTATCTGACCTGTACAAAACACATTC 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 510 actgcccagctctcgtatgaatctctggaatctgcacaactagtgagtttgatcttaac 569
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 460 CAAAGCAATCTTACCTCCACACTTGGAAATCTGAAGAACTCATGAGCTTGATCTGTAC 519
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 570 ttaaacagctctcgtgtctatctcgaatcattggaagaacttcaagctgagattt 629
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 520 AACCAACATCTTACAGAGATGTTCCACTTCTTGGGAAATTCAGTCTTGCTCTTT 579
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 630 ctccgcttaacacacacagctctcagctggttcaatctcattgcaatgaatattact 689
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 580 TTACGGCTTAATGACACCGATTTGACCGGTCCATCCCTAGAGACATCAGCGCAATCCCA 639
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 690 acccttcaagtgtagatctatcaataacagactctcgtgttcagttccctgcagaatgyc 749
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 640 GCTTTAAAGTGTGTGACGTCTCAAGCAATGATTTGTGTGGCAATCCCAACAAACGGA 699
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 750 tccctcactcttcacacccatcagtttgcataaac 788
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 700 CCCTTGTGTCACATTCCTTTACAGAACTTTGAGAACAAAC 738
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 9
T62124 standard; cDNA to mRNA; 3176 BP.
ID T62124;
AC T62124;
DT 10-JUN-1997 (first entry)
DE Arabidopsis thaliana plant morphogenesis regulatory protein cDNA.
KW plant; morphogenesis; regulation; short; stem; alteration;
KW inflorescence; extraneous; gene; expression; transformation;
KW increase; control; form; length; ds.
OS Arabidopsis thaliana.
FH Key Location/Qualifiers
FT CDS 51..2981
    /tag=a
    /note="plant morphogenesis regulatory protein"
PN J09056382-A.
PD 04-MAR-1997.
PR 24-AUG-1995; 216187.
PR 24-AUG-1995; JP-216187.
PA (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
PA (CHIK-) ZH CHIKYU KANKYO SANGYO GIYUTSU KENKYU.
DR WPI: 97-206629/19.
DR P-PADB: W13408.
PT DNA encoding plant morphogenesis regulatory protein - useful to
PT yield plants with short stems or altered inflorescence
PS Claim 1; Pages 6-10; 17pp; Japanese.
CC The present sequence encodes an Arabidopsis thaliana plant
CC morphogenesis regulatory protein (MRP), which can be used to yield
CC a plant with, e.g. short stems or altered inflorescence. The MRP
CC acts on a plant at a specific site for a specific period, and can
CC therefore be used to regulate extraneous gene expression in a
CC plant. The MRP's cDNA or genomic DNA can be used to transform a
CC plant to increase its MRP expression, and therefore control the
CC form (particularly stem length) of the plant.
SQ Sequence 3176 BP; 927 A; 654 C; 659 G; 936 T;

Query Match 7.9%; Score 165.6; DB 1; Length 3176;
Best Local Similarity 49.2%; Pred. No. 3e-36;
Matches 643; Conservative 0; Mismatches 619; Indels 46; Gaps 6;

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QY 411 agagtgtattggggaatgcagagattatctggtccattagttccagagattgtgtc 470
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1341 ACATTTGATCTTCCACACACAGATTAATGAAATTCCTTCTTCCCTTGCTATTTG 1400
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Db 2303 TGGCCTTCCCTCCACCAATAGTTCATCCCAACATCATACCGGAGCATGAAATCAAGCA 2362  
QY 1495 acatcctcttaagcagaagaatttcgaagcggttcttggaatttcgggttcgcaaaactta 1554  
Db 2363 ACCTGCTCTTCTGACGAATATCTGATGCGCTACCTATGGAATTTGGAAAGCGCGGCTCG 2422  
QY 1555 tggactataaagcaccatcgcgttac--aacagcagtcgctgcacatcgatcacatcg 1611  
Db 2423 TGAATGCTGTGACTCACAATCTAACCGTGAAGAGCTCTTAGAACAACCTGGTTATGTGG 2482  
QY 1612 ctccagaatactctcaaccggaanaactctcagagaanaaacgacgcttttcgatacggaa 1671  
Db 2483 CTCCCAAGTACTTCCAGTGGTATTTGGACAACACTAAGGCGCAGCTACAGCTAATGGCG 2542  
QY 1672 tcatgcttctagactaactcaacgagaagaagcttgcgctgcgtcgtcagctaaag 1731  
Db 2543 TTGTTCTTCTGGAGCTTCTCTCAGGAAAAAACCAATCAATCCGACTGAAAT----- 2595  
QY 1732 acgacgacgtcatgttacttgaactggtgtaagagattglttgagaagagaagctagaga 1791  
Db 2595 -CGGCGACAAATATCTCATCGACTGGGCGCAAGCAGATGGTTAAGAGAGACCGGTGCAGCG 2653  
QY 1792 tgttagtgcagaccagatctc--aaacaactacgagagagaagactgcgaacagtga 1848  
Db 2654 AGATATTTTGCATCTTATTTGACCGCACAAAAATCTGCGAGTGCAGCTGTACAGTATC 2713  
QY 1849 tacaagtgcgttgcctatgcagcagaagatcaccaatggaagaagcaagaagtctgaag 1908  
Db 2714 TGGCGATGCTGTCGCCAGTGGCTTGGAGATCAACCTAGTGCAGACCTACAGATGATCCAG 2773  
QY 1909 ttgtaaggaatgct 1921  
Db 2774 TCATGGCAATGTT 2786

RESULT 11  
X23533  
ID X23533 standard; DNA; 3842 BP.  
AC X23533;  
DT 17-JUN-1999 (first entry)  
DE Tomato Xa21 clone TRK2 DNA fragment.  
KW Xa21; receptor kinase-like protein; multigene family; RRR; rice; TRK2;  
KM plant disease resistance; cassava; maize; tomato; Xanthomonas; ss.  
OS Lycopersicon esculentum.  
PN M0909151-A2.  
PD 25-FEB-1999.  
PE 17-JUL-1998; 014841.  
PR 13-AUG-1997; US-910386.  
PA (REGC ) UNIV CALIFORNIA.  
PI Hulbert SH, Richter T, Ronald PC, Song W, Szabo V,  
PI Wang G;  
DR WPI; 99-204431/17.  
DR P-PSDB; W23533.  
PT New RRR polynucleotides and nucleic acid constructs - used for  
PT generating transgenic plants resistant to Xanthomonas  
PS Claim 14; Page 61-62; 67pp; English  
CC This invention describes a method for conferring disease resistance in  
CC plants. The invention describes the use of novel genes and proteins  
CC belonging to the Oryza longistaminata and Oryza sativa receptor  
CC kinase-like protein (RRK) Xa21 multigene family. Such genes from  
CC cassava, maize and tomato are also described. The genes and proteins can  
CC be used for enhancing resistance to Xanthomonas in a plant, preferably in  
CC rice or tomato.  
SQ Sequence 3842 BP; 984 A; 719 C; 894 G; 1244 T;

Query Match 6.8%; Score 142.6; DB 1; Length 3842;  
Best Local Similarity 46.0%; Pred. No. 8 6e-30;  
Matches 682; Conservative 0; Mismatches 774; Indels 25; Gaps 5;

QY 459 ctgtgtgtcctcaagaatttcagatcttgagccttacagtaacacataactgccc 518  
Db 2039 CTGGCCAGATTAAGGATCTCACTTCTCTTGGTGGCAATTAATCTGGTGGCCCA 2098

QY 519 attcctagtaacttgggaatctgacaactagtgagtttgatcttacttaaacagc 578  
Db 2099 ATCCCTCAAGTTTGGCCAAATGCACTTTGAAAAGCTTTGAAAGCTTTGCAATTTCT 2158  
QY 579 tctccggttccattccggaaatcattggaaagcttccaagctgagatcttcctcggtc 638  
Db 2159 TTGCTGTGGTGAATTCCAAAATATCTGTAATTTGAGGAATTTTGACTCTCTTCTCTG 2218  
QY 639 aacaacacagctcactggttcaattcctatgtaactgacaalatatactaccctcaa 698  
Db 2219 AACACAACAATTTATTCAGGGAATAATACCTTCAGGCTTGCCAAATGAGACACTGGCA 2278  
QY 699 gtgttagatcataaataaagaactctcgttgcagttcctgtaaatgctcctctca 758  
Db 2279 GCATTTAAGTTCCTTTCAATATCTGCTGGCCACTGCTCTTACCAAAAGATTTATG 2338  
QY 759 ctctcacacccatcagtttgtaataactagaccatgtgacccgttacaagtcac 818  
Db 2339 AAGTGTATATGTTTCAGGGAACCCCTTTCTGCAATGTCCTCATGTTTCTCTATCA 2398  
QY 819 ccaatgctggaatctccccc-----tttctctccacacccttlatcaactccc 872  
Db 2399 ACACCTTCTACAGATCACAGGGAAGATAGGGAGACTCAAGATTCGTGCGTCTCCT 2458  
QY 873 ccaatttccaccccgagtggtatgtatactg-----gagcaatactggtgga 923  
Db 2459 TCAGGTTCAACCCCAAGAGGAGGAGCGAGCTTCAACTCCATAGATGATGCCATCA 2518  
QY 924 gtgtcgtcaggtgctgcttgccttgcctcgtcctcgtgaatgacttgcgttggtgcga 983  
Db 2519 ACATCTCGGCGAGCTATTTGTGCACTTCTTCTGCTGATAGTCGTCTTTTAAACC 2578  
QY 984 cgaagaagcccaactagatatcttctcgaatgctccgcgaagaagatccgaatctcat 1043  
Db 2579 AGAAATGGAATCCAAGATCTAGAGTGTCTGATCTACAGAAAGAAAGTGCAGAGTGT 2638  
QY 1044 ctggagacagctcaagaagtttctcttgcgagagctacaagtggcgagtgtatgtagt 1103  
Db 2639 ACAGAAGTTCGGGTTCTTTTAAATGAAATGATGCGGCGCACAGGAGCTTCAAT 2698  
QY 1104 aacaagaacatttggcagagagtggttggaaagctcacaagagagcttgagagac 1163  
Db 2699 GCAACCAATTCATAGGAGAGTGGAGGTTTGGAGCAACATCAAAAGCGAGATTTGCCA 2758  
QY 1164 ggaactctgttctgltcaagaagctgaaagaagacgaactccaggtgagagctccag 1223  
Db 2759 GGGTTCCTAGTGCAGTAAGAGGACTTCTGTAGGAGCTTTTC--AGGGATTCACACAG 2815  
QY 1224 ttcaacaagaagttagatgataatgtagcagttcatcgaaaccgtgtgagattcga 1283  
Db 2816 TTTGATGCAAGAAATCAGAACTGGGGAGGCTTCGACATCCAAACCTCGTAACCTCATATA 2875  
QY 1284 ggttctgtaigaacgcgacgagagatgcttgtgtaaccttaacatgagcaatggaagt 1343  
Db 2876 GCATTTCAATATGGAACACGAATGTTTCTGATCTTAATCTTTTCCAGGTGTAAT 2935  
QY 1344 gtgtctgltgltcagaagaagccacgcgttcaacaactccgcttgattgccaacg 1403  
Db 2936 TTGGAAGATTATTCAGAGAG-----GTCACAAAGGCGTGGACGTGAGGTTCTT 2989  
QY 1404 aagagaatcgcgttagctcagctcgcaggttgttcttaacctaatgatactgcgacgcg 1463  
Db 2990 CACAAGATGCTTTGGATGTAGCCCTGCTCACTTCTTACCTGCAATGATGATGTGTACCA 3049  
QY 1464 aagatcattcacccgtgagcgttaaagcagaacacatcccttaagcagaagaattcgaagcg 1523  
Db 3050 CGTGTGCTTCACTCGATGTGAAGCCGACCAACTTTTATTGGATGAGAGATTAATGCA 3109  
QY 1524 gtgttgagatttccggttggcaaaacttaaggactataaagaacacatccgttgcacaca 1583  
Db 3110 TATTATCTGAATTTGTTGGTGAATGATTAAGTGGAACTTCAGAGACCCATGCAACTACT 3169

QY	1584	gdcgtccgttgcacccaatcogtcaatcagttccagaatattcttcaacgcggaattctta	16433
Db	3170	GGTGTGGCGGGAACTTTTGGATATGTGGCTCCCGAATATGACATACCTTGGCCGCTCTCG	32299
QY	1644	gagaaaaacgcagcgttttcgatacggaaatcaatgcttctcgaactaatcacaggaacaaaga	17033
Db	3230	GACACAGCGCTATGTCTCTACAGTTATATGGGGTGTGGTCTTGATTAATATACAGATATAGAA	32899
QY	1704	gcttcgatctcgctgcgcagtaagtaacgcagcgcagacgtatgtaactgaactgaggttgaa	17633
Db	3290	GCACTAATACCGTCCTTCTCTTTCTTTATGGAAATGATTTAAATTTGTACTTTGGGCATGC	33499
QY	1764	ggaattgttgaagagagaagacgtagatgattagtgatgcagatcttcaaacaaataac	18233
Db	3350	ATGCTTTTACGCGACGGCCGCTGTACAGAGATCTTTACGGCTCTGTATATGGATTTACGTC	34099
QY	1824	gagagagagaaactggaacaaatgatacaagtgcgcttgctatlgacgcgaagaatcacca	18833
Db	3410	CACATGAT - GATTTGGATATAGGTCCTACACATTCCTGGCAGTGTGTGCACGGTTACCTCTTT	34688
QY	1884	atggaagaaccaaagaatgcttgaagtttgaagaatgctgga	1924
Db	3469	TCTACTAGACCAACAATGAAGCAAGTAAGTAAGACGGTTTAA	3509

RESULT	12
ID	X07356 standard; DNA; 4104 BP.
AC	X07356;
DT	21-MAY-1999 (first entry)
DE	Arabidopsis steroid receptor Bin1 DNA.
KM	Bin1, steroid receptor; receptor kinase; transgenic plant;
KM	brassinosteroid; disease resistance; crop protection;
KM	contraceptive; ss.
OS	Arabidopsis thaliana.
FT	location/Qualifiers
FT	97..3687
FT	CDS
FT	/*tag= a
FN	W09859039-A1.
PD	30-DEC-1998.
PE	24-JUN-1998; U03100.
PR	24-JUN-1997; US-881706.
PA	(SALK ) SALK INST BIOLOGICAL STUDIES.
PI	Chory J, Li J;
DR	WPI; 99-081275/07.
P-PSDB;	W97819.
PT	New receptor kinase Bin1 involved in brassinolide signalling -
PT	useful for promoting increased yield and disease resistance in
PT	plants and for modulating oocyte maturation
PS	Claim 8: Page 49-52; 72pp: English.
CC	This DNA sequence codes for a novel plant steroid receptor kinase,
CC	designated Bin1 (see W97819), which is involved in the pathway for
CC	the synthesis of the plant steroid hormone, brassinolide. 18 New
CC	Arabidopsis dwarf mutants were identified that lacked the ability
CC	to respond to brassinolide, and were named Bin mutants. The Bin1
CC	mutations were used to map the gene to a small interval on
CC	Arabidopsis chromosome 4. Bin1 was cloned by map-based cloning.
CC	The Bin1 polynucleotide was identified within this interval by
CC	sequencing the wild-type and mutant alleles of this nucleic acid.
CC	Overexpression of Bin1 in transgenic plants provides plants
CC	characterised as having enhanced disease resistance, increased
CC	plant yield or vegetative biomass and increased seed yield.
CC	Expression of Bin1 may also increase resistance to pesticides.
CC	Inhibition of Bin1, e.g. using antisense oligonucleotides (AON), is
CC	used to render plants male-sterile, and to reduce their stature or
CC	yield, e.g. for creating dwarf varieties. Since Bin1 homologues
CC	may be involved in regulation of the menstrual cycle and uterine
CC	function, Bin1, antibodies and AON may be useful as contraceptives
CC	for improving success of in vitro fertilisation and to prevent
CC	premature labour. Transgenic animals are also provided, and are
CC	models for studying steroid-receptor interactions or can be used
CC	to screen for therapeutic agents.
SQ	Sequence 4104 BP: 1061 A; 870 C; 930 G; 1243 T;

Query Match	6.7%	Score 139.6;	DB 1;	Length 4104;
Best Local Similarity	52.9%	Pred. No. 6.1e-29;		
Matches 348;	Conservative	0;	Mismatches 304;	Indels 6; Gaps 2;

OY	1058	gaggtttctcttcgcggaagctacaagtgcgcggtgtagtggtttagtaacaagaacattt	1117
Db	2703	GAACCTCACGTTTGGATCTTTCTTCAGGCTACCAATGGTTTCCAAATGATGCTCAT	2762
OY	1118	ggcagaggtgtggttttgggaaagtctcaacaaggacgcttgcgacacggaaacctgttcg	1177
Db	2763	TGGTTCTGCTGGTGGTTTGGAGATGTTTACAAAGCGATTGTTGAAAGATGGAAGCGCGTGC	2822
OY	1178	tgtcaagaagactgaagaagaacgcaactccaggttggagaagctccagtttcaacagaagt	1237
Db	2823	TATCAGAGAACTGTATTCATGTTATGCGGTCAAGT---GATGAGAGGTTTCATGCGGAAT	2879
OY	1238	agaagatgaatgaatgttgcagtttcgaacacgcttggagatctagcaggtttctgtatgc	1297
Db	2880	GGAAACCATTTGGGAAATCCAAACATCGAAATCTTGTCCTCTTCTTGGTTATGCAAAAT	2939
OY	1298	accgaccgagagattgtcttgatctcttaacatgycgaatggaaagtgtgtcttgcgtc	1357
Db	2940	TGGAGACGAGCGGCTTCTTGTATGAGTTATGAAGTATGAGAACTTTGAAGATGTTT	2999
OY	1358	cagagagagagcgaactcacaacctccgcttgaatttggccaacgcggaagaatccgcct	1417
Db	3000	GCAAGACCCCAAGMAAGGTGGGGTGAACCTTAATTTGTCCACACGCGGGAAGATTCGAT	3059
OY	1418	aggctcaagctcgagttctgtcttaacctacaatgacatgcgatccgaagatcatcacg	1477
Db	3060	AGGATCACTGAGAGGGTTGCTTTCCTTCACCAACACTGCAGTCGCGATCATCATCACAAG	3119
OY	1478	tgaacgtaaagcagcaaacatccctcttagacgagaatcgaagcggttgttggagattc	1537
Db	3120	AGACATCGAAATCCAGTATGTTGTGCTGATGGAATTTGGAAAGCTCGGGTTTCAGATTT	3179
OY	1538	cgggtttgcgaagtcttgactatataaagacatcccgga---caacagcgctccggtg	1594
Db	3180	TGGCGTGGCGGGCTGATGATGTCGATGGGATPACGCAATTTAAAGCTCAGTACATTAGCTGG	3239
OY	1595	caccatcggtacacatcgtccagaatattcctcaacggaanaatcttcagagaaacga	1654
Db	3240	TACACCGGGTTAGCTTCTCTCCAGAGATTACCAAAGTTTCAGGTGTTCAACAAAGAGAGA	3299
OY	1655	cgcttccgatacggaaatcatgctcttagaactaatcaacagacaagaagcctttgat	1712
Db	3300	CGTTATAGTTAGTCGTGTGCTTACTCGAGCTACACGGGTAAACGCCCAAGCAT	3357

RESULT 13

T31307

ID T31307 standard; cDNA; 1554 BP.

AC T31307;

DE 15-NOV-1996 (first entry)

DE Tomato RRR gene clone TRK1.

KW Xa21; RRR; disease resistance; Xanthomonas; blight; rice;

KM tomato receptor kinase 1; TRK1; transgenic plant; crop protection;

KW ss.

OS Lycopersicon esculentum.

PN M09622375-A2.

PD 25-JUL-1996.

PE 17-JAN-1996; U00717.

PR 17-JAN-1995; US-373374.

PR 07-JUN-1995; US-475891.

PR 29-SEP-1995; US-004645.

PA (REGC ) UNIV CALIFORNIA.

PI Ronald PC, Song W, Szabo V, Wang G;

DR WPI: 96-354532/35.

DR P-PSDB; W03186.

PT plant disease resistance gene Xa21, codes for RRR polypeptide -

PR useful for conferring resistance to Xanthomonas in rice and tomatoes



QY 1633 gaaaattctcagagaaaaccgacgttttcgatacgaatcatcgtctctgaactaatca 1692  
||| | ||||| | | | | | | | | | | | | | | | | |  
Db 2652 TGAATAATTGATGAGAAAAGCGATGTATAGCTTTGGAGTGGTGTGAGCTTATAA 2711  
1693 caggacaaagagcttcgactcgtcgtcgaactaagcagcagcgtcatgttacttg 1752  
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1753 actgggtgaaaagattgttgaaggagaagaagctagaagatgttagtgcagatctc 1812  
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Db 2772 AAACGAGACAAATGAGCAAGAGGGGTGTGAAAAATCTTG-----ATGAGAGGC 2825  
1813 aaacaactacgaagagaagaactgtgaacaagtacacaaagtggcggttgcatagcgc 1872  
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Db 2826 TTAATAAATGTTGCAATGTTGTAAGCTATGCAAGATATTTTGTAGCAATGCTTTGTGTG 2885  
1873 aaggatcaccaatggaagaccaaagattgtctgaagtgtgaagatgct 1921  
||| | | | | | | | | | | | | | | | | | | | | | | | |  
Db 2886 AAGAGTACAGCATGTAGAGGCGCTACAAATGAGGGAAGTAGTCCAATGCT 2934

RESULT 15  
ID T62125 standard; DNA; 9295 BP.  
AC T62125;  
DT 10-JUN-1997 (first entry)  
DE Arabidopsis thaliana plant morphogenesis regulatory protein DNA.  
KW Plant; morphogenesis; regulation; short; stem; alteration;  
infiorecence; extraneous; gene; expression; transformation;  
increase; control; form; length; ds.  
OS Arabidopsis thaliana.  
FH key  
FT exon Location/Qualifiers  
FT 1803..1881  
FT /\*tag= a  
FT 1882..2227  
FT /\*tag= b  
FT 2228..2366  
FT /\*tag= c  
FT 2367..2467  
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FT 2540..2643  
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FT 6012..6095  
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FT 6520..5412  
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FT 6891..6974  
FT /\*tag= az  
FT 6975..7328  
FT /\*tag= ba  
FT exon  
FT J09056382-A.  
FT PD 04-MAR-1997.  
FT PF 24-AUG-1995; 216187.  
FT PA (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.  
FT PA (CHIK-) 2H CHIKYU KANKYO SANGYO GIJITSU KENKYU.  
FT DR WPI; 97-206629/19.

PT DNA encoding plant morphogenesis regulatory protein - useful to  
PT yield plants with short stems or altered inflorescence  
PS Claim 6; Pages 12-15; 17pp; Japanese.  
CC The present sequence encodes an Arabidopsis thaliana plant  
CC morphogenesis regulatory protein (MRP), which can be used to yield  
CC a plant with, e.g. short stems or altered inflorescence. The MRP  
CC acts on a plant at a specific site for a specific period, and can  
CC therefore be used to regulate extraneous gene expression in a  
CC plant. The MRP's cDNA or genomic DNA can be used to transform a  
CC plant to increase its MRP expression, and therefore control the  
CC form (particularly stem length) of the plant.  
SQ Sequence 9295 BP; 2873 A; 1581 C; 1602 G; 3239 T;

Query Match 5.5%; Score 114.4; DB 1; Length 9295;  
Best Local Similarity 56.7%; Pred. No. 9.8e-22;  
Matches 211; Conservative 0; Mismatches 161; Indels 0; Gaps 0;  
QY 1345 ttgttcggtctcagagagagccacgctcacacctccgcttattgccaagcgga 1404  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
6499 ttgcttgggtgtttttaaagccctaacgaagaaaaagacttgaattggacacgac 6558  
QY 1405 agagaatcgcgtcagagctcagaggttgccttaccatgatcactgcgaccca 1464  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
6559 ttaagatgacatattggtgacgacacaggtttagcttatctacacacatgactgtaccca 6618  
QY 1465 agatcattcacgctgacgtaaaagcagaacatccctcttagagcgaagaattcgagcg 1524  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
6619 ggatcatttcacagagacgtgaagtcgtccacattcttggacaaagactttagagcgtc 6678  
QY 1525 ttgttgagatttcggggttcgcaagcttatgactataaagacactcagtgacacag 1584  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
6679 gtttgacacatttttgcaatagcgaagaaagcttggtgtgtcgaagtcacatcttcaactt 6738  
QY 1585 cagtcggtgcacacatcggtcacatcgctccagaatattctcaacgcygaaatcttcag 1644  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
6739 acgtgatgggacagataggttacctagaccgagatctctgcacttcacggtcactcg 6798  
QY 1645 agaaacgcgacgttttcgatacgcgatacatcttcttagaactaatcagaagacaagag 1704  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
6799 agaaatccagatgcttacagttatggaatagctcttcttgattgttaaccgaagaaag 6858  
QY 1705 cttcgactcgt 1716  
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
6859 ccgtgatgacg 6870

Search completed: June 23, 2000, 22:54:50  
Job time: 40686 sec



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2000, 19:06:46 ; Search time 6198.48 Seconds  
(without alignments)  
1366.010 Million cell updates/sec

Title: US-09-180-798-32

Perfect score: 2089

Sequence: 1 ggatttattattttttt.....taaaaaaaaaaaaaaaaaa 2089

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4857316 seqs, 202661650 residues

Total number of hits satisfying chosen parameters: 9714632

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_est1:\*  
2: em\_est2:\*  
3: em\_est3:\*  
4: em\_est4:\*  
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7: em\_est7:\*  
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17: em\_est17:\*  
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64: gb\_est38:\*  
65: em\_est27:\*  
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80: gb\_est46:\*  
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84: gb\_gss3:\*  
85: gb\_gss4:\*  
86: em\_gss1:\*  
87: em\_gss2:\*  
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105: gb\_gss12:\*  
106: gb\_gss13:\*  
107: gb\_gss14:\*  
108: gb\_gss15:\*  
109: gb\_gss16:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result

Query

SUMMARIES





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QY	1869	acgcaagaatcacccaatggaagaagaccaaagatgtctgaagtgtgaagatgcttgaaga	1928
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ACCESSION	AA738547	656 bp	mRNA
VERSION	AA738547.1	GI:3421472	
KEYWORDS	EST.		
SOURCE	Sorghum bicolor		
ORGANISM	Sorghum bicolor		
REFERENCE	Amnen, F., Chang, J.-L., Paterson, A. H. and Stockhaus, J.		
AUTHORS	Amnen, F., Chang, J.-L., Paterson, A. H. and Stockhaus, J.		
TITLE	Characterization of 14 different putative protein kinase cDNA clones of the C4 plant Sorghum bicolor		
JOURNAL	Mol. Gen. Genet. 259 (1), 115-122 (1998)		
MEDLINE	98409267		
COMMENT	On Nov 29, 1993 this sequence version replaced gi:636097.		
	Contact: Stockhaus J		
	Institut fuer Entwicklungsbiologie und Molekularbiologie der Pflanzen		
	Heinrich-Heine-Universitaet		
	Universitaetsstrasse 1, 40225 Duesseldorf, Germany		
	Tel: (49)-211-81-14953		
	Fax: (49)-211-81-14871		
	Email: stockha@uni-duesseldorf.de		
FEATURES	Insert Length: 1100	Std Error: 0.00.	
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	Site_2: Xho I; leaf cDNA library from green leaves,		
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QY	1339	gaagtgatgcttcgtgtcctcagagagagagccacgcgtcaacactccgcgttga-----c	1395					
Db	62	GGAGTGTGGCATCACGTTTACGAGAGGACAGCAATCTGACCCACTGTTAAGTGGAAA	121					
QY	1336	caacgcggaagaagaatcgcgtcgtacgtcgaactcgaagttgtgtcttaacctatgacac	1455					
Db	122	CMAAGAGAGAGCGGATTCGCGCTGGATGTGTCMAAGAGAGACTTTCCTACTGCATGATCACT	181					
QY	1456	gcgcgcgaagaatcattcacccgcgcgaagtaaagacacaaactccctcttagcgaagaa	1515					
Db	182	GGGATCCCAATATATCATTCGGGATCTCAAACTCCAAATATCTTCTTCATAGAGACT	241					
QY	1516	tcgaagcggttgtgttgagattccgggtgtgcaagcttatgactataaagaacactcacg	1575					
Db	242	TCGAGGCGAGTTGTGGTGATTTTGGGCTTGCCAAAGCTTATGAGACTCAAAAGTATCCATG	301					
QY	1576	tgacaacagcagtcctcgtgacacatcgcgtacatcgcctcagaatactctctaaccgaa	1635					
Db	302	TCACAACATGCTGTCCGTTGGAACAATTGACACATTCGCGCTGATGCTCATTCACATGCGCA	361					
QY	1636	aattcttaagaagaacccgaagtttctcggatagaagaaatctatgctcttaagaactaatcaag	1695					
Db	362	AGTCTCTGAAAAACATCGATGATTTTGGCTATGAGATCATGCTCTGAGCTTATTAATCTG	421					
QY	1696	gacaaagagcttcgcgtatcgcctcgcgtacgaagacacagcagcgtcatgtaactgact	1755					
Db	422	GCCAGAGGGCATTTGATCTTGCTGCTGCTTCCAAATATGATGCAATGTATGCTTCTTGACT	481					
QY	1756	gggtgaaagatgtgttgaaagagaaagaagctatgatatgtatgtatgatacagatcttcaaa	1815					
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QY	1816	caaatctacgagagagagagacttggaaacagtgtataaagtgtgcgtgttcatacgaacag	1875					
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LOCUS	SBRLK3 Sorghum bicolor cv. TX430 leaf Sorghum bicolor cDNA clone							
DEFINITION	SBRLK3 similar to protein kinase, highest similarity to receptor-like protein kinases, mRNA sequence.							
ACCESSION	AA738545							
VERSION	AA738545.1							
KEYWORDS	EST.							
SOURCE	Sorghum.							
ORGANISM	Sorghum bicolor							
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REFERENCE	1 (bases 1 to 1435)							
AUTHORS	Annen, F., Chang, J.-L., Paterson, A. H. and Stockhaus, J.							
TITLE	Characterization of 14 different putative protein kinase cDNA clones of the C4 plant Sorghum bicolor							
JOURNAL	Mol. Gen. Genet. 259 (1), 115-122 (1998)							
MEDLINE	98409267							
COMMENT	On Nov 29, 1993 this sequence version replaced gi:636085.							
	Contact: Stockhaus J							
	Institut fuer Entwicklungsbiologie und Molekularbiologie der Pflanzen							
	Heinrich-Heine-Universitaet							
	Universitaetsstrasse 1, 40225 Duesseldorf, Germany							
	Tel.: (49)-211-81-14953							
	Fax: (49)-211-81-14871							
	Email: stockhaeuni-duesseldorf.de							

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		Site_2: Xho I; Leaf cDNA library from green leaves,			
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OY	1141 tctacaaggagcgttcgcaagcagcaactctgttgtcgtcgaagagctcgaaggagagc	1200			
Dd	557 TATATAAAGGACCACCTTCCAGATGGCACCTAGAATTGCCTGTAAACGGTTAACTGATTACG	616			
OY	1201 gaaccceagtgtagagctccagttccaacaagaagttagatgaataagtcagcttc	1260			
Dd	617 AAAGTCCTGGTAGAAGGCTGCTTCTTCGCCGAGAGTTGACGTGATGTGTGCAGTTTC	676			
OY	1261 atcgaaacctgttgagatcacgagtlctcgtlatgacacgcagccagagattgcttgt	1320			
Dd	677 ACCGGAATCTTTTAAGATTGATTGGTTCTGTCTGTACAACAACAACAGAGCGCCTGCTTGT	736			
OY	1321 atccctaacatgccaatggaagtgttgtctcgtctcagaagaagagccacgctcaaac	1380			
Dd	737 AACCTTTATCATGACGAAATCTTACTGTGGCCCTACCGCTTACGAGA---ATTAACTGGGACC	793			
OY	1381 ctccgcttgattggccaacgcggaagagagatccgcgtagagctcagctcgaagtttgtct	1440			
Dd	794 CAATTATTAATTGGTCTCTGCAGGAAGAACGAGTGGCTATTAGGCCACAGCTCCTGGACATGGAGT	853			
OY	1441 accctaatgatcatcgcatccgaagatcatccacgctgacgtlaaagaagcagaacaatcc	1500			
Dd	854 ATTTGCAGACGACATGCATCTTAAGATTATATCATATCGTACGTCACAAAGCGTCCCAATGTCT	913			
OY	1501 tcttagaagaagaatctcgaagcgttgttgttgagattcgggttggcgaagcttaaggact	1560			
Dd	914 TGCTTGATGTAAGGTTTTGAACCGGTATGTTGGATTTCCGCTTGGCCAAGCTGGAGAG	973			
OY	1561 ataagaacatcacgtgacaacagcagatccgtcyggaaccaatcgttacatcgtccgaat	1620			
Dd	974 TACAAAGACATCTGTGGCTGCTCAGGTCGTGGAACTATGGGTCAATATGCCCTCGAAT	1033			
OY	1621 atcttcaaccggaaaatcttcagaagaaaaacgcagcttttcggatacggaaatcatgcttc	1680			
Dd	1034 ATTGTCCACACTGGGAATGCATCCGAGAGAACCGAATGTTTGTGTTAACGGCATTAATATGCTTC	1093			
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Dd	1094 TCGACCTAGTCACTGCTGGCTGGCTGCATTATGATCTTTTTCACAGTCTGG---AGGAAGAAGATG	1150			
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OY	1801 atccagatcttcaacaacaactlacgcggagagagaagaaatgaaacaagtgaatacaagtgcgt	1860			
Dd	1211 ACCGTAACCTGAACAAATTTTCAACGGCGCAGAGAGTGGAGATGATGATCAACCATGATCGGCC	1270			
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DB	1271	TGCTGTGCACGAGGCTTCGCTTAGAGACCGGCGCTCCATGTCGAGGTGTCGCGATGC	1330
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DB	1331	TGGAAGGCGAGGCGCTCGACAGAGAGTGGAGAGATGCGACAGCAGCTGAGGTGAGGAGG	1389
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DEFINITION	AlT28030	555 bp mRNA EST	11-JUN-1999
ACCESSION	AlT28030	BNGH19629 six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to (U93048) somatic embryogenesis receptor-like kinase [Daucus carota], mRNA sequence.	
VERSION	AlT28030		
KEYWORDS	AlT28030.1	GI:5046816	
SOURCE	EST.		
ORGANISM	Gossypium hirsutum	upland cotton.	
REFERENCE	Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euglylliphytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids II; Malvales; Malvaceae; Gossypium.		
AUTHORS	1 (bases 1 to 555)		
TITLE	Blewitt, M., Matz, E.C., Davy, D.F. and Burr, B.		
JOURNAL	ESTs from developing cotton fiber		
COMMENT	Unpublished (1999)		
	On Jun 5, 1998 this sequence version replaced gi:3187310.		
	Contact: Ben Burr		
	Biology Department		
	Brookhaven National Laboratory		
	Upton, NY 11973, USA		
	Tel: 516-344-3396		
	Fax: 516-344-3407		
	Email: burr@nslu1.dnl.gov		
	Seq primer: T3 Primer.		
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Best Local Similarity	76.2%; Pred. No. 1.4e-77;		
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DB	61	CGGCTGTGACGTGCGACATGTCGACATATTGCCCGAGATATCTCTACTGTAATCTT	120
OY	1642	cagagaaaaacgagcttctcgatagcgaatcatgctcttagaactatcacaggacaa	1701
DB	121	CAGAGAAAACCTGATGTTTGGGTATGATGATCATCTTTGGAGCTTAACTGCAGAC	180
OY	1702	gagcttctgactcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc	1761
DB	181	GCGCCTTGTGATCTCTCGCTTGTGCAATGATGATGATGATGATGATGATGATGATG	240
OY	1762	aaggaattgtgaagagaagaagctcagaagatcttagttagatccagatctcaacaa	1821
DB	241	AAGGACTTCTGAGAGAGAAAAGCTGGAATTTCTTGTGATCTGATCTGATCTGCAACCAAT	300

QY	1822	acgsggaggaagacacggaacaaagatatacaagatggcgttctatgcacggaagatcac	1881
Db	301	ATGTAGAAACTGTAAGTTAAAGCACTTAATCAAGCTTGCTCTCTATGCAACAAAGGTTCC	360
QY	1882	caatggaagaaccgaagatgtctcgaattgttaagagatctcgaagaagatggcttcg	1941
Db	361	CAATGACACCGCCAAAGATGTCTGAAGTGTGTTAAATGCTGGAAAGTGAAGTGTGGCCG	420
QY	1942	agaatgtggcgaatggcaaaaagttgagatcttgaagggaagatgattgaagtccta	2001
Db	421	AAATATGGATGATGAGTGGCAGAAAGTTGAAGTTCTACGGCAGACAGATGCAACTTCCCTC	480
QY	2002	atccaaacttgatctgattcttgatctcactcactcaattgcacgccttgatctatc	2061
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ACCESSION	AW233982		
VERSION	AW233982.1	GI:6566309	
KEYWORDS	EST.		
SOURCE	soybean.		
ORGANISM	Glycine max		
REFERENCE	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.		
AUTHORS	1 (Phases 1 to 532)		
TITLE	Shoemaker, R., Keim, P., Vodkin, L., Erpelting, D., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, V., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schuck, R., Ritter, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.		
JOURNAL	Public Soybean EST Project		
COMMENT	Unpublished (1999) On Feb 18, 1999 this sequence version replaced gi:4297707. Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or Info@genomesystems.com web site: www.genomesystems.com High quality sequence stop: 403. Location/Qualifiers 1..532 /organism="Glycine max" /db_xref="taxon:3847" /clone="GENOME SYSTEMS CLONE ID: Gm-cl028-1713" /clone_11b="Gm-cl028" /tissue_type="roots of 'Supernod' plants" /lab_host="DH10B" /note="Vector: pBluescript II XR; Site.1: EcoRI; Site.2: XhoI. The mRNA was isolated from roots of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were inoculated with Bradyrhizobium japonicum, strain USDA110 prior to harvest. StrataGene's cDNA synthesis kit (catalog number 200401) was used to		
FEATURES			
SOURCE			

			synchronize the cDNA. First-strand synthesis was performed with 5'-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V-A-C, or G) was added to the 3' end of the primer [GAGAGAAGAGAGAGAGAGAACACTGCAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase, ligated to EcoRI adaptors and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's Bluescript II XR pre-digested vector (Bluescript II SK(+)) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (~25). This library was constructed by Dr. Paul Keim and Dr. Virginia Corryell."		
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2	CATCGTAATTTCCTTGGCTTGCGGTTCGTGGTTTGTATGACACCACACGAACGTTGCTTGG 61				
QY 1320	tatctcttaacatggccaatggaaagtgttccttggtctcagaagagagccacgcgtcaaa 1379				
62	TATCCTTCAATGGCTAAACGGAAGTGTAGCATATGTTTACGGAACGTCMAAATCCCAA 121				
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QY 1440	taacctaatgatcactgcgatcgatcgaagatcattcaatccgtgacgttaaaaagcagcaaacatc 1499				
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362	TACCTTCCTCAACTGGAAAGCTTTCACAGAAAGACTGATGTTTTTGGATTGCTGTGATGCTT 421				
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422	CTTGAACATAATNAACGCAAAAGGGCTTTTGAATCTAGCTCGACTTGGCCATATATATGAT 481				
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RESULT 6					
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LOCUS					
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Db	309	TTTGACACAGGTCACACGTGCAATTGATTTCCACGCTTGGAAGATGAAGATGATGTTCTGC	368
Qy	1747	tacttgactgggtgaaagatcgtgtgaagagaagaagcttagagatglttagtgcacag	1806
Db	369	TTCTTGACTATGTCAAAAACCTGGAAAAGGAGAAAACCTGGATGCTATCTAGATCATTA	428
Qy	1807	atcttcaaaccaactaagagagagagaagaaacttgaaacaagtgtatacaagtgaggttgcat	1866
Db	429	ATCTTAATAAAAAATTACCAATGGAGGACGTTAACCAATGATCCAAAGTTGCAATTCCTT	488
Qy	1867	gcaacgaagatccaccaaatggaaagacaaagaatgctgaagttgtaagaatgcgtgaaag	1926
Db	489	GCACCCCGACCTCCCAAAAAGAACCTCCGGGAATTTTCGAGGTTGTAAGAACTCTGGAG	548
Qy	1927	gagatggccttcggagagaatggga	1951
Db	549	GAACAAGGCTCTCCCAAGAGTGA	573

RESULT	11
LOCUS	A1486453
DEFINITION	EST244774 tomato ovary, TAMU Lycopersicon esculentum cDNA clone CLE98c2, mRNA sequence.
ACCESSION	A1486453
VERSION	A1486453.1 GI:4381824
KEYWORDS	EST.
SOURCE	tomato.
ORGANISM	Lycopersicon esculentum Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Euarchytophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
REFERENCE	1 (bases 1 to 471)
AUTHORS	Alcala,J., Vredalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato carpel tissue Unpublished (1999) On May 7, 1998 this sequence version replaced gi:3121325.
TITLE	JOURNAL
COMMENT	

Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 4366  
Fax: 864 656 4293  
Email: drfisch@clemson.edu.  
Location/Qualifiers  
1. .471

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/cultivar="TA496"
/db_xref="taxon:4081"
/clone="CLE08G2"
/clone_lib="tomato ovary, TAMU"
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/dev_stage="5 days pre-anthesis to 5 days post-anthesis"
/lab_host="X11-Blue MRF"
/notes="Vector: pBlueScript SK(-); Site_1: EcoRI; Site_2:
XhoI; cLED - Tomato Carpel EST library. OligodT-primed and
directionally cloned cDNA in vector lambda ZAP II with 5'
and 3' ends located at the EcoRI and XhoI sites,
respectively."

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## ORIGIN

Query Match	10.7%;	Score 222.8;	DB 47;	Length 471;
Best Local Similarity	67.4%;	Pred. No. 5.6e-47;		
Matches 314;	Conservative	0;	Mismatches 152;	Indels 0;
			Gaps	0;

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RESULT	12
LOCUS	A1416897
DEFINITION	A1416897 474 bp mRNA EST 01-DEC-1999 Gm-cl005.x1 Gm-cl005 glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl005-165.3', similar to TR-O23921 023921 SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE. ;, mRNA sequence.
ACCESSION	A1416897
VERSION	A1416897.1
KEYWORDS	GI:4260401
SOURCE	EST.
ORGANISM	soybean. glycine max

REFERENCE AUTHORS	TITLE
1 (bases 1 to 474) Shoemaker, R., Keim, P., Vodkin, L., Erpelidg, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.	euphylliplopytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycyne.
Unpublished (1999)	Public soybean EST Project
On May 7, 1998 this sequence version replaced gi:3119924.	

Contact: Shoemaker R/Public Soybean EST Project  
Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: estewatson.wustl.edu





```

RESULT 14
AI487272 568 bp mRNA EST 29-JUN-1999
LOCUS EST245594 tomato ovary, TAMU Lycopersicon esculentum cDNA clone
DEFINITION cLED11M7, mRNA sequence.
ACCESSION AI487272
VERSION AI487272.1 GI:4382643
KEYWORDS EST.
SOURCE tomato.
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 568)
REFERENCE 1
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T.,
Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B.,
Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C.,
Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato carpel tissue
Unpublished (1999)
On May 18, 1998 this sequence version replaced gi:3136952.
CONTACT: David Frisch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4366
Fax: 864 656 4293
Email: dfisch@CLEMSON.EDU.
LOCATION/Qualifiers
FEATURES
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and 3' ends located at the EcoRI and XhoI sites,
respectively."
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Matches 312; Conservative 0; Mismatches 169; Indels 0; Gaps 0;
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QY 327 aatgctctgagagctggaatcctacgctgagatcctggaacatgctcagatcact 386
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 148 AATGTTCTCAAAAGCTGGGACCTTACACTTGTAATCCTTGACATGGTTTCAATGTTACC 207
QY 387 tgaacaacagagacagtgatcataagagttgattgagggaatgacagatctatcgccat 446
|| || || || || || || || || || || || || || || || || || || || ||
DB 208 TGTGACTCAAGATATATATGTTATTCGCTGGGCAATTCATATATTTCTGSAACA 267
QY 447 ttatgtccagagctgtgtgtctcaagaattgcagatttgagattgacgttaacaac 506
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QY 507 atatacggccagatctctagtaatactggaactgacaacactagtgattgattcctt 566
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QY 567 tacttaacagcttcccggtccattcccggaatcatctgggaagaagcttcaagctgaga 626
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QY 627 ttcttcgcggtctaacacaacagctcactcagtggttcattctctatgcatcagaccattt 686
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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DEFINITION T2E10-T7 TAMU Arabidopsis thaliana genomic clone T2E10, genomic
survey sequence.
ACCESSION B09168
VERSION B09168.1 GI:2090299
KEYWORDS GSS.
SOURCE thale cress.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
Arabidopsis.
1 (bases 1 to 1202)
REFERENCE 1
Feng,J., Dewar,K., Buehler,E., Kim,C., Li,Y., Shinn,P., Sun,H. and
Ecker,J.
BAC End Sequences at ATGC
Unpublished (1997)
Other GSSs: T2E10-Sp6
CONTACT: Ecker J.
Arabidopsis Thaliana Genome Center
University of Pennsylvania
Dept. of Biology, University of Pennsylvania, Philadelphia, PA
19104
Tel: 215-898-9384
Fax: 215-898-8780
Email: jecker@atgenome.bio.upenn.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 76
High quality sequence stop: 704.
LOCATION/Qualifiers
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Matches 273; Conservative 0; Mismatches 90; Indels 1; Gaps 1;
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DB 339 TAATTTTCAATTCGTGATGATGACCGAGAGAGATCTCTGAGTTCACTTGGGCGACACTTA 398
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Db 399 AGCGTTCTCTCTACGGGAACCTCAAGTANCACTGATACCTTCAGCAACAAACATTT 458
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Db 459 TGGGCCGAGGTGGGTTCGGAAGTCTACAAAGGCCCTCTTGCTGATGGAACACTGTGTG 518
QY 1177 ctgtcaagagacttgaagaaagagcgaaactccaggttgaagagctccagttcaaacagaag 1236
Db 519 CAGTCAAAACGGCTTAAAGAAAGAGCGAACCCAGGTGGCGAGCTCCAGTTTCAGACAGAAAG 578
QY 1237 taagatgataagatagtcagttcatcgaacctgttgagattacgaagttctgtatg- 1296
Db 579 TGGAGATGATTAGCATGGCCGCTTCACAGATATCTCTCAGGCTTACNTGGGTCTGATGGA 638
QY 1296 acaccgaaccgaagatctgtctgtatccttacatggccaatgaaagtgtgtcgtg 1355
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